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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:52:02 ; Search time 19.29 Seconds
(without alignments)
723.227 Million cell updates/sec

Title: US-09-442-143-4

Perfect score: 2340

Sequence: 1 MRLPGWLSSAVLACRAV.....GYKSFSKQAKMIRKNEKP 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2340	100.0	432	1	FIBX_MOUSE
2	493.5	21.1	463	1	FIBB_CHICK
3	488.5	20.9	437	1	FIBG_HUMAN
4	488.5	20.9	453	1	FIBH_HUMAN
5	470.5	20.1	477	1	FIBB_PETMA
6	466	19.9	444	1	FIBG_BOVIN
7	463.5	19.8	282	1	FIBG_FARPA
8	463	19.8	491	1	FIBB_HUMAN
9	459	19.6	468	1	FIBB_BOVIN
10	454	19.4	866	1	FIBB_HUMAN
11	452	19.3	782	1	FIBB_RAT
12	448.5	19.2	438	1	FIBG_XENLA
13	444	19.0	479	1	FIBB_RAT
14	435	18.6	445	1	FIBG_RAT
15	431.5	18.4	741	1	FIBB_CHICK
16	426.5	18.2	432	1	FIBG_PETMA
17	417	17.8	255	1	MF44_HUMAN
18	416.5	17.8	1808	1	TERA_CHICK
19	414.5	17.7	4289	1	TERX_HUMAN
20	408.5	17.5	1746	1	TERA_PIG
21	406.5	17.4	2201	1	TERA_HUMAN
22	377	16.1	541	1	FIB2_PETMA
23	372.5	15.9	774	1	SCA_DROME
24	190.5	8.1	129	1	MF44_BOVIN
25	110	4.7	304	1	MMGL_MOUSE
26	110	4.7	876	1	MYSS_HUMAN
27	109.5	4.7	1940	1	MYSE_HUMAN
28	108	4.6	1805	1	HMW2_MYCGE
29	106.5	4.6	1957	1	YD86_SCHPO
30	106	4.5	1940	1	MYSE_RAT
31	105.5	4.5	692	1	MYSP_ODCA
32	105	4.5	872	1	TE95_TETTH
33	105	4.5	1102	1	MYSC_CHICK

34	104.5	4.5	455	1	VIME_CYPCA
35	104.5	4.5	507	1	VLI_HPV37
36	104.5	4.5	1607	1	LMG1_MOUSE
37	104.5	4.5	1878	1	BRC1_CANFA
38	102.5	4.4	1300	1	DYNA_NEUCR
39	101.5	4.3	1940	1	MYSE_CHICK
40	101	4.3	1250	1	BXE_CLOBO
41	100.5	4.3	579	1	G160_HUMAN
42	100.5	4.3	950	1	Y136_HUMAN
43	100.5	4.3	1107	1	VJEP_ECOLI
44	100	4.3	450	1	VIMB_CARAU
45	100	4.3	3433	1	UTRO_HUMAN

ALIGNMENTS

RESULT 1	
FIBX_MOUSE	
ID	FIBX_MOUSE STANDARD; PRT; 432 AA.
AC	P12804;
DT	01-OCT-1989 (Rel. 12, Created)
DT	01-OCT-1989 (Rel. 12, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	PROTHROMBINASE PRECURSOR (FIBRINOGEN-LIKE PROTEIN) (CYTOTOXIC T-DE
DE	LYMPHOCYTE SPECIFIC PROTEIN).
GN	FIBLP OR FGL2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=CYTOTOXIC T-CELL;
RA	MEDLINE=87115527; Pubmed=3550794;
RT	Koyama T., Hall L.R., Hasegawa W.G., Toneyawa S., Saito H.;
RT	"Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT	homology to fibrinogen beta and gamma chains.";
RL	Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
RN	[2]
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC	STRAIN=BALB/CJ; TISSUE=PERITONEAL MACROPHAGE;
RA	MEDLINE=95333285; Pubmed=7609073;
RA	Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
RA	Levy G.;
RT	"Association of mouse fibrinogen-like protein with murine hepatitis
RT	virus-induced prothrombinase activity.";
RL	J. Virol. 69:5033-5038(1995).
CC	-1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC	-1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC	T-CELLS.
CC	-1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
CC	VIRUS STRAIN 3 (MHV-3).
CC	-1- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC	THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
CC	-----
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CC	-----
DR	EMBL; M16238; AAA37624.1;
DR	EMBL; M15761; AAA37624.1; JOINED.
DR	EMBL; S78773; AAB34823.1;
DR	PIR; A27447; A27447.
DR	HSP; P02671; 1FZD.
DR	MGI; M103266; FGL2.
DR	INTERPRO; IPR002181;
DR	PFAM; PF00147; fibrinogen_C; 1.
DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW	T-cell; Cytolysis; Blood coagulation; Signal.

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FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 432 PROTHROMBINASE.
FT DISULFID 206 235 BY SIMILARITY.
FT - DISULFID 364 377 BY SIMILARITY.
FT CONFLICT 332 332 A -> G (IN REF. 2).
SQ SEQUENCE 432 AA; 48951 MW; 2B297F69CCBA4782 CRC64;

Query Match 100.0%; Score 2340; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPGWLWLSAVLAACRAVEHNTEGLEDSAAQACPARLEGSGRCGSCPTQLTLP 60
DB 1 MRLPGWLWLSAVLAACRAVEHNTEGLEDSAAQACPARLEGSGRCGSCPTQLTLP 60
QY 61 TLTQLPROLGSMEEVRLKEAVRLKKAQVLSKKSCODCKLOADHRDPGGNGGGAETAED 120
DB 61 TLTQLPROLGSMEEVRLKEAVRLKKAQVLSKKSCODCKLOADHRDPGGNGGGAETAED 120
QY 121 SRVQELSSQVNLKSLSELNAKDOIQLQGLRLETLHLVNMNNIENYVDNKVANLTVVNSL 180
DB 121 SRVQELSSQVNLKSLSELNAKDOIQLQGLRLETLHLVNMNNIENYVDNKVANLTVVNSL 180
QY 181 DGKSKCPSQEHMQSQPVHLYKDCSHYVGLGRSSGAYRVTDPHRNSSFEVYCDMETM 240
DB 181 DGKSKCPSQEHMQSQPVHLYKDCSHYVGLGRSSGAYRVTDPHRNSSFEVYCDMETM 240
QY 241 GGGWTVLQARLDGSGNFTREWKDYKAGFNGLEREFLWGNKDKIHLTKSEMILRIDLEDF 300
DB 241 GGGWTVLQARLDGSGNFTREWKDYKAGFNGLEREFLWGNKDKIHLTKSEMILRIDLEDF 300
QY 301 NGLTYALYDQFYVANEFLKYLHIGNYNGTAGDALRFSRHHYNDLRFPTTPDRNDRYP 360
DB 301 NGLTYALYDQFYVANEFLKYLHIGNYNGTAGDALRFSRHHYNDLRFPTTPDRNDRYP 360
QY 361 SGNGLYSSGWWFDCSLANLNGYHOKYKGVNRGIFGWTPGNGAQPGYKSSFKO 420
DB 361 SGNGLYSSGWWFDCSLANLNGYHOKYKGVNRGIFGWTPGNGAQPGYKSSFKO 420
QY 421 AKMIRPKNFKP 432
DB 421 AKMIRPKNFKP 432

RESULT 2
FIBB_CHECK
ID FIBB_CHECK STANDARD; PRT: 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN BETA CHAIN PRECURSOR (FRAGMENT).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RT cleavage site."
RL Biochemistry 30:3290-3294(1991).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
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CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -----
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CC -----
DB EMBL; M58514; AAA48770.1; -
DR PIR; A38463; A38463.
DR HSSP; P02675; 1FZB.
DR INTERPRO; IPR002181; -
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfatation.
FT PEPTIDE 1 17 FIBRINOPEPTIDE B.
FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.
FT MOD_RES 5 5 SULFATATION (BY SIMILARITY).
FT SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
FT FIBRINOPEPTIDE B).
FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 205 289 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 397 410 BY SIMILARITY.
FT CARBOHYD 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;

Query Match 21.1%; Score 493.5; DB 1; Length 463;
Best Local Similarity 30.4%; Pred. No. 8.2e-29;
Matches 137; Conservative 58; Mismatches 162; Indels 93; Gaps 14;

QY 30 EDASAAQAACPARLEGSGRCE-----GSCQPFQLTTLPTLTQLPROLGSMEEVLKEVRTL 83
DB 51 QDQAMKKKGPIIYPDAGGCKHPIDELGVLCPTGCELOT-----TLKKQKTV 97
QY 84 KEAVDSLKKSCQDCKLOADHRDPGGNGGGAETAEDSRVQELSSQVNLKSLSELKNARDQ 143
DB 98 KPVLRDLK-----DRVAKFSD-----TSTMYQYVNMIDNKLKLVTKQKQKDN 139
QY 144 ---IQLOGRLFTLHLVNMNNIENYVDNKVANLTVVNSLGDGKCKSPQEHMQSQ----- 196
DB 140 DIILSEYNTMELHNYIKDNLNNIPSSLRVLRVAVDSLHKKIKLENAIATQDTCRS 199
QY 197 -----PVHLYTKDCSHYVGLGRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQ 248
DB 200 PCVASCNIPV--VSGRECEDIYRKGGETSEMYIIQPPFTTPYVYCDMETGGWTVLIQ 257
QY 249 ARLDGSTNFTREWKDYKAGFNGLER-----EFLWGNKDKIHLTKSEMILRIDL 297
DB 258 NRQDGSVNGFRAMDEYKRGFNIAKSGGKVKYCDTPGVEVLGNDKISQITKIGPTKVLIE 317
QY 298 EDFNGLTLYALYDQFYVANEFLKYLHIGNYNGTAGDALR--FSRHYN-----HDLRF 348
DB 318 EDWNGKRVSAVYGGFTTHNEGKRYQLSVSNYKGNAGNALMEGASQLYCENTRTMTIHNGMY 377
QY 349 FTTTPDRNDRY-----PSGNCGLYSSGWWFDCSLANLNGY-----HOKYKGVNRG 397
DB 378 FSTYDRNDGWLTFDPRKQCKSKEDGGGWWYNRCHAANPNRGYYWGTYSWDMAKHGTDG 437
QY 398 IFWGTWPGINQAQPGYKSSFKQAKMIRP 427
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Db 438 IVVMNWKG-----SWY--SWKKMSMKIKP 459

RESULT 3

FIBG HUMAN STANDARD; PRT; 437 AA.

AC P02679;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE FIBRINOGEN GAMMA-A CHAIN PRECURSOR.

GN FGG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RX SEQUENCE FROM N.A.

RX MEDLINE=85252774; PubMed=2990550;

RA Rixon M.W., Chung D.W., Davie E.W.;

RT "Nucleotide sequence of the gene for the gamma chain of human fibrinogen.";

RL Biochemistry 24:2077-2086(1985).

RN [2]

RX SEQUENCE FROM N.A.

RX MEDLINE=83283434; PubMed=6688357;

RA Chung D.W., Chan W.-Y., Davie E.W.;

RT "Characterization of a complementary deoxyribonucleic acid coding for the gamma chain of human fibrinogen.";

RL Biochemistry 22:3250-3256(1983).

RN [3]

RX SEQUENCE OF 27-437.

RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;

RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural variants.";

RL (In) Peeters H. (eds.);

RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56, Pergamon Press, Oxford (1980).

RN [4]

RX SEQUENCE OF 75-286 FROM N.A.

RC TISSUE=LIVER;

RX MEDLINE=92119334; PubMed=1685103;

RA Marchetti L., Zanelli T., Malcovati M., Tenchini M.L.;

RT "Polymorphism of the human gamma chain fibrinogen gene.";

RL DNA Seq. 1:419-422(1991).

RN [5]

RX SEQUENCE OF 285-437 FROM N.A.

RX MEDLINE=85030379; PubMed=6092346;

RA Fornace A.J., Jr., Cummings D.E., Comeau C.M., Kant J.A., Crabtree G.R.;

RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the 3' end of the gene produces gamma A and gamma B forms of gamma-fibrinogen.";

RL J. Biol. Chem. 259:12826-12830(1984).

RN [6]

RX SEQUENCE OF 209-270 FROM N.A.

RX MEDLINE=84069777; PubMed=6689067;

RA Inam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;

RT "Isolation and characterisation of cDNA clones for the A alpha- and gamma-chains of human fibrinogen.";

RL Nucleic Acids Res. 11:7427-7434(1983).

RN [7]

RX REVIEW, AND DISULFIDE BONDS.

RX MEDLINE=83254370; PubMed=6575689;

RA Henschen A., Lottspeich F., Kehl M., Southan C.;

RT "Covalent structure of fibrinogen.";

RL Ann. N.Y. Acad. Sci. 408:28-43(1983).

RN [8]

RX DISULFIDE BONDS.

RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A., Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;

RT "The structures of fibrinogen and fibrin.";

RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K., Neurath H. (eds.);

RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172, Pergamon Press, New York (1978).

RN [9]

RX DISULFIDE BONDS.

RX MEDLINE=76225080; PubMed=936108;

RA Blomback B., Hessel B., Hogg D.;

RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";

RL Thromb. Res. 8:639-658(1976).

RN [10]

RX QUATERNARY STRUCTURE, AND DISULFIDE BONDS.

RX MEDLINE=83231465; PubMed=6860649;

RA Hoeprich P.D., Doolittle R.F.;

RT "Dimeric half-molecules of human fibrinogen are joined through disulfide bonds in an antiparallel orientation.";

RL Biochemistry 22:2049-2055(1983).

RN [11]

RX REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.

RX MEDLINE=84305751; PubMed=6383194;

RA Doolittle R.F.;

RT "Fibrinogen and fibrin.";

RL Annu. Rev. Biochem. 53:195-229(1984).

RN [12]

RX POLYMERIZATION SITE.

RX MEDLINE=85014892; PubMed=6592597;

RA Horwitz B.H., Varadi A., Scheraga H.A.;

RT "Localization of a fibrin gamma-chain polymerization site within segment Thr-374 to Glu-396 of human fibrinogen.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).

RN [13]

RX POLYMERIZATION SITE.

RX MEDLINE=81142375; PubMed=6451630;

RA Oleksa S.A., Budzynski A.Z.;

RT "Localization of a fibrin polymerization site.";

RL J. Biol. Chem. 256:3544-3549(1981).

RN [14]

RX PLATELET AGGREGATION SITE.

RX MEDLINE=84203545; PubMed=6326808;

RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;

RT "Platelet receptor recognition site on human fibrinogen. Synthesis and structure-function relationship of peptides corresponding to the carboxy-terminal segment of the gamma chain.";

RL Biochemistry 23:1767-1774(1984).

RN [15]

RX PLATELET AGGREGATION SITE.

RX MEDLINE=84185664; PubMed=6325435;

RA Plow E.F., Srouji A.H., Meyer D., Marguerie G., Ginsberg M.H.;

RT "Evidence that three adhesive proteins interact with a common recognition site on activated platelets.";

RL J. Biol. Chem. 259:5388-5391(1984).

RN [16]

RX CALCIUM-BINDING SITE.

RX MEDLINE=85261382; PubMed=3160702;

RA Dang C.V., Ebert R.F., Bell W.R.;

RT "Localization of a fibrinogen calcium binding site between gamma-subunit positions 311 and 336 by terbium fluorescence.";

RL J. Biol. Chem. 260:9713-9719(1985).

RN [17]

RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.

RX MEDLINE=97169449; PubMed=9016719;

RA Yee V.C., Pratt K.P., Cote H.C.F., Le Trong I., Chung D.W., Davie E.W., Stenkamp R.E., Teller D.C.;

RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma chain of human fibrinogen.";

RL Structure 5:125-138(1997).

RN [18]

RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.

RX MEDLINE=97352771; PubMed=9207064;

RA Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;

RT "The primary fibrin polymerization pocket: three-dimensional structure of a 30-kDa C-terminal gamma chain fragment complexed with the peptide Gly-Pro-Arg-Pro.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).

RN [19]

[illegible]

RX MEDLINE=87146483; PubMed=3029722;
 RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RT beta gene.";
 RN Nucleic Acids Res. 15:1615-1625(1987).
 [8]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RA Acta Chem. Scand. 19:1788-1789(1965).
 [9]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschel A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RA Ann. N.Y. Acad. Sci. 408:28-43(1983).
 [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=7724599; PubMed=891553;
 RA Gardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RT disulfide-containing cyanogen-bromide fragments.";
 RA Eur. J. Biochem. 77:595-610(1977).
 [11]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RA (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RA Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 [12]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RA Annu. Rev. Biochem. 53:195-229(1984).
 [13]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE=97472408; PubMed=933233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RT crosslinked counterpart from fibrin.";
 RA Nature 389:455-462(1997).
 [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RA Biochemistry 37:8637-8642(1998).
 [15]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RA Biochemistry 38:2941-2946(1999).
 [16]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE=89058942; PubMed=3194892;
 RA Schmelzer C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RT structural studies of fibrinogen Baltimore II.";
 RA Thromb. Res. 52:173-177(1988).
 [17]
 RP VARIANT ISE.
 RX MEDLINE=91208409; PubMed=2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the

RT replacement of B beta glycine-15 by cysteine.";
 RA Blood 77:1958-1963(1991).
 [18]
 RP VARIANT NAPLES.
 RX MEDLINE=92340664; PubMed=1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
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 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -!- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -----
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 DR EMBL: J00133; -; NOT_ANNOTATED_CDS.
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 DR EMBL: M64983; AAA18024.2; -;
 DR EMBL: M26877; AAA52445.1; -;
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 DR PDB: 1FZH; 08-JUN-99.
 DR PDB: 1FZI; 08-JUN-99.
 DR PDB: 1FZJ; 08-JUN-99.
 DR PDB: 1FZK; 08-JUN-99.
 DR PDB: 1FZL; 08-JUN-99.
 DR PDB: 1FZM; 08-JUN-99.
 DR PDB: 1FZN; 08-JUN-99.
 DR PDB: 1FZO; 08-JUN-99.
 DR PDB: 1FZP; 08-JUN-99.
 DR PDB: 1FZQ; 08-JUN-99.
 DR PDB: 1FZR; 08-JUN-99.
 DR PDB: 1FZS; 08-JUN-99.
 DR PDB: 1FZT; 08-JUN-99.
 DR PDB: 1FZU; 08-JUN-99.


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DR INTERPRO: IPR002181; -
DR PFAM: PF00147; fibrinogen_C; 1.

Query Match      19.8%; Score 463; DB 1; Length 491;
Best Local Similarity 28.4%; Pred. No. 1.5e-26;
Matches 131; Conservative 60; Mismatches 151; Indels 120; Gaps 13;

OY 32 ASAAQACPARLEGSGRCGSCQFQTLPTLTITOLPRLGSMEEVLKRVTLKRAVDSLK 91
Db 79 AATQKKVERKAPDAGGLHAD-----PDLGVLCPTGCGQLQEAALLQQRPIRNSDELN 131
OY 92 KSCDCKLQADHRDPGGNGNGAETADS-----RVQELSVQNKLS 135
Db 132 NNVEAV-----SOTSSSFQYMYLLKDLWQKROKOVKDNENYVYSS 174
OY 136 ELKNADKQIOGLQGLRLETLHLVNMNNIENVDNKV-----ANLTVVVNSLDGKCKSPSQ 190
Db 175 ELE--KHQL-----YIDETVNSNIPNLRLVLSILENLSKIQKL 212
OY 191 EHMOSQPVH-----LIYKDCSDHYVYGLRRSGAYRVTPDHRNSSFEVYCDM 237
Db 213 ESDVSAOMEYCRTPCTVSCNIPVSGKECEIIRKGGSETSEMYLIQPDSSVKPYRVYCDM 272
OY 238 ETWGGGWTVLQARLDGSTNTRWKDYKAGFGN-----LRREFWLGNDKTHLL 285
Db 273 NTENGCGWTVIQNRQDGSVDFGRKWDYPYKQGFNVATNTDGNKYCGLPGEYWLGNDKISQL 332
OY 286 TSKSEMILRDLDEENGLTLYALYDQFYVANFLKYLHIGNYNGTAGDALRFSRHY--- 342
Db 333 TRMGPTLEIEMEDGDKGVKAHYGGFTVONEANKYQISVKNKYRGTAGNALMDGASOLMG 392
OY 343 -----NHDLRFPTTDPDRNDRY-----PSGNCGLYYSWGWFDSCLSANLNGKY--- 387
Db 393 ENRTMTIHNCMFSTYDRNDGHLTSDPRKQCKSKEDGGGWHYNRCHNPNRGYYWGQY 452
OY 388 --HQYKGYRNGIFWGTWPIQNAQPGYKSPKQAKMIRP 427
Db 453 TWDMAKHGTDGQVVMNWKG-----SWY--SMRKMSMKIRP 486

RESULT 9
FIBB_BOVIN
ID FIBB_BOVIN STANDARD; PRT; 468 AA.
AC P02676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN BETA CHAIN.
GN FGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP Sjoquist J., Blomback B., Wallen P.;
RA "The sequence of amino acids at the N-terminal end of bovine
RT fibrinopeptide B.;"
RL Acta Chem. Scand. 17:1816-1819(1963).
RN [2]
RP SEQUENCE OF 5-21.
RA Sjoquist J., Blomback B., Wallen P.;
RT "Amino acid sequence of bovine fibrinopeptides.;"
RL Ark. kemi 16:425-436(1960).
RN [3]
RP SEQUENCE OF 22-53.
RX MEDLINE=79164394; PubMed=434821;
RA Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
RT "Amino acid sequences of portions of the alpha and beta chains of
RT bovine fibrinogen.;"
RL Arch. Biochem. Biophys. 192:27-32(1979).
RN [4]
```

SEQUENCE OF 44-468 FROM N.A.
MEDLINE=81199473; PubMed=6262803;
Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
"Characterization of a cDNA clone coding for the beta chain of bovine
fibrinogen.;"
Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
-!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
-!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
(STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
MONOMERS.

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EMBL; V00110; CAA23444.1; -
PIR; A03122; FGBOB.
HSSP; P02675; 1FZA.
INTERPRO: IPR002181; -
PFAM: PF00147; fibrinogen_C; 1.
PROSITE; PS00514; Fibrin_Ag_C_Domain; 1.
Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
PEPTIDE 1 21 FIBRINOPEPTIDE B.
FT CHAIN 22 468 FIBRINOGEN BETA CHAIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 6 6 SULFATATION.
FT SITE 21 22 CLEAVAGE (BY THROMBIN; RELEASE
FIBRINOPEPTIDE B).
FT DISULFID 72 72 INTERCHAIN (WITH ALPHA).
FT DISULFID 83 83 INTERCHAIN (WITH ALPHA).
FT DISULFID 87 87 INTERCHAIN (WITH GAMMA).
FT DISULFID 200 200 INTERCHAIN (WITH ALPHA).
FT DISULFID 204 204 INTERCHAIN (WITH GAMMA).
FT DISULFID 208 293 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 401 414 BY SIMILARITY.
FT CARBOHYD 371 371 N-LINKED (GLCNAC...) (PROBABLE).
SQ SEQUENCE 468 AA; 53340 MW; 2DBD42F443AA4B37 CRC64;

Query Match 19.6%; Score 459; DB 1; Length 468;
Best Local Similarity 28.5%; Pred. No. 2.7e-26;
Matches 123; Conservative 57; Mismatches 150; Indels 102; Gaps 11;

OY 50 GSQCFFQLTPTLTITOLPRLGSMEEVLKRVTLKRAVDSLKSCDCKLQADHRDPGG 109
Db 80 GVLCPGCKLQDTLVRQER-----PIRKSIEDLRNTVDSVSR----- 117
OY 110 NGNGCAET-----AEDSRVQELSVQNKLSSELKNKAKDIOGLQGLRLETLHLV 157
Db 118 -----SSSTFOYITLLKNMKWGRQNVQDNVYVNEYSSHLEKHOLYID----- 161
OY 158 NMNNIENVYDNKVANLTVVNSLDGKCKSPSOEHMSQPVHLLYKDCSDHYVGLR--- 214
Db 162 --ETVKNNIPTKLRVLRSLLENLRSLKIOKLESVDSTOMEYICRTPCTVTCTNIPVSGKECE 219
OY 215 -----RSSGAYRVTPDHRNSSFEVYCDMETWGGGWTVLQARLDGSTNTRWKDYKAG 267
Db 220 KIIRNEGETSEMYLIQPEDSSKPYRVYCDMKTGKGTWVIQNRQDGSVDFGRKWDYPYKOG 279

QY 268 FGNLER-----EFWLGNDKIHLLTKSKEMILRIDLEFNGLTLYALYQFYVA 315
 DB 280 FGNATNAEGKKYCGVPGYEWLGNDRIQSOLNMGPTKLLIEMEDKNGDKVTYALYEGFTVQ 339
 QY 316 NEFLKYLRIHIGNYTAGDAL-----RFSRHYNDLRFETTPDRDNDRY-----PSG 362
 DB 340 NEANKYQLSVSKYKTAGNALIEGASQLVGENRTFTIHSMEFFSYDRDNGKWTDPK 399
 QY 363 NCGLYYSGWFDSCLSANLNGKYY-----HOKYKGVNRGIFWGTWPGINQAQPGGYK 415
 DB 400 QCSKEDGGWYNRCHAANPNRGYWGAYTWDMAKHGTTDDGVVNMNMG-----SWY- 452
 QY 416 SSFKQAKMIRP 427
 DB 453 -SMKKMSMKIRP 463

RESULT 10
 FIBA_HUMAN
 ID FIBA_HUMAN STANDARD; PRT; 866 AA.
 AC P02671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
 GN FGA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A. (ALPHA-E FORM).
 RX MEDLINE=93090725; PubMed=1457396;
 RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
 RA Roy S.N., Redman C.M., Griening G.;
 RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
 subunit: a novel exon conferring marked homology to beta and gamma
 subunits.";
 RT Biochemistry 31:11968-11972(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ALPHA-E FORM).
 RA Chung D.W., Griening G.;
 RL (In) Ebert R.F. (eds.);
 RL Index of variant human fibrinogens, pp.13-24, CRC Press,
 RL Boca Raton (1994).
 RN [3]
 RP SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
 RC TISSUE=LIVER;
 RX MEDLINE=91344740; PubMed=2102623;
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 fibrinogen.";
 RL Adv. Exp. Med. Biol. 281:39-48(1990).
 RN [4]
 RP SEQUENCE FROM N.A. (ALPHA FORM).
 RX MEDLINE=83247396; PubMed=6575389;
 RA Kant J.A., Lord S.T., Crabtree G.R.;
 RT "Partial mRNA sequences for human A alpha, B beta, and gamma
 fibrinogen chains: evolutionary and functional implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
 RN [5]
 RP SEQUENCE OF 1-629 FROM N.A.
 RX MEDLINE=83283432; PubMed=6688355;
 RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 the alpha chain of human fibrinogen.";
 RL Biochemistry 22:3237-3244(1983).
 RN [6]
 RP SEQUENCE OF 20-629.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 structural variants.";
 RL (In) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,

RL Pergamon Press, Oxford (1980).
 RN [7]
 RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
 RX MEDLINE=80088231; PubMed=518846;
 RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 overlapping sequences providing the complete sequence.";
 RL Biochemistry 18:5410-5416(1979).
 RN [8]
 RP SEQUENCE OF 110-156 FROM N.A.
 RX MEDLINE=84069777; PubMed=6689067;
 RA Inam A.M., Eaton M.A., Williamson R., Humphries S.;
 RT "Isolation and characterization of cDNA clones for the A alpha- and
 gamma-chains of human fibrinogen.";
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [9]
 RP SEQUENCE OF 605-644 FROM N.A. (ALPHA FORM).
 RX MEDLINE=83254384; PubMed=6575700;
 RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
 RT "Cloning of fibrinogen genes and their cDNA.";
 RL Ann. N.Y. Acad. Sci. 408:449-456(1983).
 RN [10]
 RP SEQUENCE OF 20-35.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [11]
 RP CROSS-LINKING ACCEPTOR SITES.
 RX MEDLINE=80088230; PubMed=518845;
 RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
 RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
 Exact location of cross-linking acceptor sites.";
 RL Biochemistry 18:5405-5410(1979).
 RN [12]
 RP CROSS-LINKING ACCEPTOR SITES.
 RX MEDLINE=78130085; PubMed=632262;
 RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
 RT "Localization of the alpha-chain cross-link acceptor sites of human
 fibrin.";
 RL J. Biol. Chem. 253:2184-2195(1978).
 RN [13]
 RP VARIANT, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [14]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [15]
 RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
 RX MEDLINE=87057190; PubMed=2877981;
 RA Kimura S., Aoki N.;
 RT "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
 RL J. Biol. Chem. 261:15591-15595(1986).
 RN [16]
 RP PHOSPHORYLATION.
 RX MEDLINE=84104274; PubMed=6318767;
 RA Itarte E., Plana M., Guasch M.D., Martos C.;
 RT "Phosphorylation of fibrinogen by casein kinase 1.";
 RL Biochem. Biophys. Res. Commun. 117:631-636(1983).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
 RX MEDLINE=92218459; PubMed=1560020;
 RA Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 RT "The structure of residues 7-16 of the A alpha-chain of human
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 RL J. Biol. Chem. 267:7911-7920(1992).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.

DR	PF00147; fibrinogen_C; l.
KW	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; l.
DW	Blood coagulation; Glycoprotein; Calcium; Plasma; Platelet; Signal.
FT	SIGNAL 1 25
FT	CHAIN 26 438
FT	FIBRINOGEN GAMMA CHAIN.
FT	DISULFID 32 32 INTERCHAIN (WITH C-33') (BY SIMILARITY).
FT	DISULFID 33 33 INTERCHAIN (WITH C-32') (BY SIMILARITY).
FT	DISULFID 43 43 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT	DISULFID 47 47 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT	DISULFID 158 158 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT	DISULFID 162 162 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT	DISULFID 176 205 BY SIMILARITY.
FT	DISULFID 349 362 BY SIMILARITY.
FT	CARBOHYD 76 76 N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE 438 AA; 50064 MW; 69B1F01BB6716F60 CRC64;

Query Match		19.2%; Score 448.5; DB 1; Length 438;
Best Local Similarity		31.9%; Pred. No. 1.5e-25;
Matches 122; Conservative 60; Mismatches 149; Indels 51; Gaps		

QY	74	EEVLKEVRTLKEAVDSLKSCQDCKLQADDDHDPGGNGGNGAETAEDSRVQELESQVNL	133
DB	58	ENVDTDLQYLENLTQLISNSTSTTTIIVHLDSGKKPATSPQTALDPTQSKTCWMKL	117
QY	134	SSELKNAKDIOIGLOGRLLETFLHLVNMMNIENYYDNKVANLVTVVNSLDGKCKCPSQEHM	193
DB	118	-TOMKNYYOYEENIL-YLOEVSSNQNKI-FLLKQKIANLEL-----QCQQ-PCRDFV	166
QY	194	QSOPVQHLLTYKCSNDHYVLRGRSSGAYRYTPDHRRNSSFEVYCDMTMGWGTVVLQARDLG	253
DB	167	Q---IQEFTGKQDEQVANKGARLSGLLYTKPLKAQQLFYCEIEPGSGSAVTIQRRLDG	223
QY	254	STNFTREWKDYKAGFG----NLEREFEWLGNDKTHLLTKSEM--ILRIDLEDFNGLTLYA	307
DB	224	SVNFHKMWQYRGFGYLSPNDKTEFWLGNEXIHLLSTOSTIPYVMRIELEDMSNQKSTA	283
QY	308	LYDQFYVANEFLRYLRLHIGNY-NGTAGDAL-----RFSRHYNHDLRAFFTFPPDRD	355
DB	284	DYSTFRLGSEKDNRYTYAFYIGGDAGDAFDGDFGDDPSDXF-YTSHGQGFSTFDKD	341
QY	356	NDRYPGNCGLYYSYGWFDFCSLANLNKYHH-----QKYKGVNRGIFWGTWPGIN	407
DB	342	NDRKF-DGNCAGEQDGSGWMNRCHAAHLNGKYGGTYSEADSPSGYDNGLIWATW----	396
QY	408	QAQPGGYKSSFKQAKMWIREPN 429	
DB	397	--RRRWY--SMKSVTMKIMPLN 414	

RESULT 13	
ID	FIBB_RAT
ID	FIBB_RAT STANDARD; PRT; 479 AA.
AC	PI4480;
DT	01-JAN-1990 (Rel. 13, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DE	01-OCT-1996 (Rel. 34, Last annotation update)
DE	FIBRINOGEN BETA CHAIN PRECURSOR.
GN	FCB.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ON	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RC	MEDLINE=95143386; PubMed=7841303;
RA	Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.;
RT	"Cloning of the complete coding sequence of rat fibrinogen B beta
RT	chain cDNA; interspecies conservation of fibrin beta 15-42 primary
RT	structure.";
RL	Blood Coagul. Fibrinolysis 5:487-496(1994).
RP	[2]
RP	SEQUENCE OF I-26 FROM N.A.


```
OY 313 YVANEFKYLRLHIGNY-NGTAGDAL-----RFSRHYNHDLRFFFTTPDRDNDYRP 360
DB 292 RVGPESDKYRLTYAYFTGGDAGDFGDFGDDPSDKF--FTSHGMHFSTWMDNDKXF- 348
OY 361 SGNCGLYSSGWFDFSCLSANLNGKYH-----QXKYGVRNCFIWTGTPGINQAOFGG 413
DB 349 EGNCAEODGSGWNNKCHAGLNGVYIOGGTYSKSTPNGYDNGLIWATW----- 398
OY 414 YKS---SFKQAKMIRPKN 429
DB 399 -KTRWYSMKETTKIIPFN 416

RESULT 15
FIBAL_CHICK
ID FIBAL_CHICK STANDARD; PRT; 741 AA.
AC P14448;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
GN FGA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE OF 1-4 FROM N.A.
RA Grellinger G.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-741 FROM N.A.
RX MEDLINE=90311369; PubMed=2367530;
RA Weissbach L.; Grieninger G.;
RT "Bipartite mRNA for chicken alpha-fibrinogen potentially encodes an
RT amino acid sequence homologous to beta- and gamma-fibrinogens.";
RL proc. Natl. Acad. Sci. U.S.A. 87:5198-5202(1990).
RN [3]
RP SEQUENCE OF 19-33.
RX MEDLINE=78187470; PubMed=656462;
RA Takagi T.; Finlayson J.S.; Iwanaga S.;
RT "Amino acid sequence of chicken fibrinopeptide A.";
RL Biochim. Biophys. Acta 534:161-164(1978).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
CC PREDOMINANT FORM.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20803; AAB60686.1; JOINED.
DR EMBL; U20799; AAB60686.1; JOINED.
DR EMBL; U20800; AAB60686.1; JOINED.
DR EMBL; U20801; AAB60686.1; JOINED.
DR EMBL; U20802; AAB60686.1; JOINED.
DR EMBL; U20803; AAB60685.1; JOINED.
DR EMBL; U20799; AAB60685.1; JOINED.
DR EMBL; U20800; AAB60685.1; JOINED.
DR EMBL; U20801; AAB60685.1; JOINED.
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DR EMBL; U20802; AAB60685.1; JOINED.
DR EMBL; M34096; AAA99306.1; -.
DR EMBL; M34096; AAA99307.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IP0002181; -.
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Signal; Alternative splicing.
FT SIGNAL 1 18 FIBRINOPEPTIDE A.
FT PEPTIDE 19 33 FIBRINOGEN ALPHA-E CHAIN.
FT CHAIN 34 741 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 19 19 INTERCHAIN (WITH C-42') (BY SIMILARITY).
FT DISULFID 46 46 INTERCHAIN (WITH THE BETA CHAIN)
FT DISULFID 55 55 (BY SIMILARITY).
FT DISULFID 64 64 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 68 68 (BY SIMILARITY).
FT DISULFID 180 180 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 184 184 (BY SIMILARITY).
FT DISULFID 310 341 INTERCHAIN (WITH THE BETA CHAIN)
FT SITE 33 34 BY SIMILARITY.
FT VARSPLIC 506 509 CLEAVAGE (BY THROMBIN; RELEASE
FT VARSPLIC 510 741 FIBRINOPEPTIDE A).
FT VARSPLIC 510 741 DCDD -> GTQK (IN ISOFORM ALPHA).
FT VARSPLIC 510 741 MISSING (IN ISOFORM ALPHA).
SO SEQUENCE 741 AA; 82438 MW; A09F5F4F186DE3A6 CRC64;

Query Match 18.4%; Score 431.5; DB 1; Length 741;
Best Local Similarity 39.2%; Pred. No. 5.1e-24;
Matches 96; Conservative 39; Mismatches 77; Indels 33; Gaps 11;

OY 204 KDCSD---HYVLGRSSGAYRVTPDHRNSFEVYCDMETMGGTWTVLQARLDGSTNFTRE 260
DB 505 KDCDDIRQKHTSGAK-SGIFKIKPEGSNKVLSVYCDQETTLGGWLLIQORMDGSVNFNR 563
OY 261 WKDYKAGFGNL-----EREFWLGNDKXIHLLTKSKEMILRIDLDENGLTLIYALYDQFYVAN 316
DB 564 WQYRRRGFGSDVGKGQGLWLGNIHLITQN-DTLRLVELEDWDGNAAYAEY-IVQVGT 621
OY 317 EFLKYLRLHIGNYNGTAGDAL-----RFSRHYNHDLRFFFTTPDRDNDYPSGNCGLYSS 370
DB 622 EAGTALTVSYSYEGTAGDALVAGWLEEGSEYTSQAOMQFSTFDRDODHWEE-SCAEVYGG 680
OY 371 GWFDFSCLSANLNGKY-----YHOKYK---GVRNGIFGTWPGINQAOFGYKSSFKQAK 422
DB 681 GWNYSQQAANLNGIYYPGGHYDPYNYVPIEENGWVWIPF-----RASDY--SLKVVR 732
OY 423 WMIRP 427
DB 733 MKIRP 737
```

Search completed: February 27, 2001, 12:52:04
Job time: 235 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:50:10 ; Search time 31.84 Seconds
(without alignments)
921.265 Million cell updates/sec

Title: US-09-442-143-4
Perfect score: 2340
Sequence: 1 MRLPGWLSSAVLAACRAV.....GYKSFQAKMIRPKNFKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2340	100.0	432	2 A27447	cytotoxic T-lympho
2	2336	99.8	432	2 I56934	fibrinogen-like pr
3	1853.5	79.2	439	2 I37391	fibrinogen-like pr
4	519.5	22.2	312	2 JN0596	fibrinogen-related
5	493.5	21.1	463	2 A38463	fibrinogen beta ch
6	489.5	20.9	437	1 FGHUG	fibrinogen gamma-A
7	489.5	20.9	453	1 FGHUGB	fibrinogen gamma-B
8	470.5	20.1	479	2 A25052	fibrinogen beta ch
9	466	19.8	444	2 S05313	fibrinogen gamma-B
10	463.5	19.8	282	2 A35084	fibrinogen-related
11	463	19.8	334	2 JC5980	ficolin-A precursor
12	463	19.8	491	1 FGHUB	fibrinogen beta ch
13	458	19.6	468	1 FGHUB	fibrinogen beta ch
14	454.5	19.4	1353	1 JH0675	restrictin precurs
15	454	19.4	866	2 D44234	fibrinogen alpha c
16	448.5	19.2	438	2 A32670	fibrinogen gamma c
17	446.5	19.1	1356	2 A45445	janusin precursor,
18	436	18.6	326	2 B47172	ficolin-beta - pig
19	435	18.6	323	2 A47172	transforming growt
20	435	18.6	326	2 S61517	ficolin-1 precursor
21	426.5	18.2	432	1 FGLMGS	fibrinogen gamma c
22	420	17.9	328	2 A05299	fibrinogen beta ch
23	420	17.9	437	1 FGRFGA	fibrinogen gamma-A
24	420	17.9	445	1 FGRFGB	fibrinogen gamma-B
25	416.5	17.8	1810	1 A32230	tenascin precursor
26	414.5	17.7	3566	1 A40701	tenascin-X precursor
27	412.5	17.6	220	2 S28170	tenascin homolog -
28	412.5	17.6	417	2 S65944	tenascin-X - pig (
29	412.5	17.6	4135	2 T42629	tenascin-X - bovin

30	409	17.5	2019	1 JQ1322	tenascin precursor
31	408.5	17.5	1746	1 S19694	tenascin precursor
32	406.5	17.4	2201	2 A32160	tenascin-C - human
33	402.5	17.2	860	2 I48839	tenascin-X - mouse
34	402.5	17.2	4006	2 T09070	probable tenascin
35	395.5	16.9	1914	2 T42635	tenascin y precurs
36	374	16.0	641	1 A41932	fibrinogen alpha-I
37	372.5	15.9	774	2 A39832	scarbous locus (sc
38	372.5	15.9	774	2 S58998	scarbous protein p
39	224.5	9.6	463	2 T15876	hypothetical prote
40	200.5	8.6	915	2 T21773	hypothetical prote
41	200.5	8.6	927	2 T21772	hypothetical prote
42	189.5	8.1	127	2 PC2036	microfibril-associ
43	170	7.3	431	2 T29850	hypothetical prote
44	169	7.2	452	2 T26827	hypothetical prote
45	165.5	7.1	146	2 T32255	hypothetical prote

ALIGNMENTS

RESULT 1

A27447

cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447

R:koyama, T.; Hall, L.R.; Haser, W.G.; Toneyawa, S.; Saito, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1611, 1987

A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology

A:Reference number: A27447; MUID:87175527

A:Accession: A27447

A:Molecule type: mRNA

A:Residues: 1-432 <KOY>

A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

F:203-428/Domain: fibrinogen beta/gamma homology <PBG>

Query Match 100.0%; Score 2340; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.7e-159;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRLPGWLSSAVLAACRAVEEHNLT	TEGLEDSAAQAACPARLEGSGRCBGSQC	60
DB	1	MRLPGWLSSAVLAACRAVEEHNLT	TEGLEDSAAQAACPARLEGSGRCBGSQC	60
QY	61	TLTIQLPROIGSMEEVLKEVRTLKEAVDSL	KSCQDCKLQADHRDPGGNGGNGAETAED	120
DB	61	TLTIQLPROIGSMEEVLKEVRTLKEAVDSL	KSCQDCKLQADHRDPGGNGGNGAETAED	120
QY	121	SRVQELSSOVKNLSSELKNAKDQIQGLGRLE	TLHLVNMNNIENYVDNKVANILTVVNSL	180
DB	121	SRVQELSSOVKNLSSELKNAKDQIQGLGRLE	TLHLVNMNNIENYVDNKVANILTVVNSL	180
QY	181	DGKCKSCPQEHMQSOPVQHLIYKDCSDHY	VLGRSSGAYRVTPDHRNSSFEVYCDMETM	240
DB	181	DGKCKSCPQEHMQSOPVQHLIYKDCSDHY	VLGRSSGAYRVTPDHRNSSFEVYCDMETM	240
QY	241	GGGWTVLQARLDGSTNFTREWKDYKAGF	GNLEREPWLNKDKIHLTLKSEMILRLDLEDF	300
DB	241	GGGWTVLQARLDGSTNFTREWKDYKAGF	GNLEREPWLNKDKIHLTLKSEMILRLDLEDF	300
QY	301	NGLTLYALYDQFYVANEFLKYLRHLHIGNY	NGTAGDALRFSRHYNHDLRFTTTPDRDNDYRP	360
DB	301	NGLTLYALYDQFYVANEFLKYLRHLHIGNY	NGTAGDALRFSRHYNHDLRFTTTPDRDNDYRP	360
QY	361	SGNCGLIYSSGGWFFDSCLSANLNGKYHOKY	KGVNRGIFWGTWPGINQAQPGGYSKSFQ	420
DB	361	SGNCGLIYSSGGWFFDSCLSANLNGKYHOKY	KGVNRGIFWGTWPGINQAQPGGYSKSFQ	420
QY	421	AKMMIRPKNFKP	432	

Qy	115	AETADSRVQBELSQVNKLSSSELKNAKDQIQGLQGRLETHLVLNMNINIENYVDNKVANUT	174
Db	41	-----ETRVKQOQVKTQLQE-----NEQVFL-----DKGDEIT	70
Qy	175	VVYNSLDGKSCSKPSEHMQSQPVHLIYKDCSDHVVILGRSSGAYRVTPDHNRSSFVY	234
Db	71	VW--DLGSKRQ-----YADCEIENGDKLSGFKIKLPQSPAEFVSY	111
Qy	235	CDMETWGGGTVALQARLDGSTNETRWKYQKAGFGNLER---EFWLGNDDKIHLHFKSKRM	291
Db	112	CDMSD--GGGTVTQRRSDGSENENRCKWQYENGFGVQKHGEYVLGNKNLHFLTQDEY	170
Qy	292	ILRIDLEDFNGLTYALYDQFYVANEFELKYRLHIGNYCTAGDALRFSRH-----YNH	345
Db	171	TLKIDLADFEKNSRYAQYNFKYVGDENYELUNIGYSGTAGDLSAGNFHPVEQVWASHQ	230
Qy	346	LRFEFTTPDRNDRYPSGNCGLYSSGWWFSDCLSLANLNGKYYHQYKYG--VRNGFIWGTWP	404
Db	231	RMKESTWDRDHNY-BGNCAEEDOSGWWENRCHSANLNGVYSGPYTAKTDNGIYVYTW-	288
Qy	405	GINOAPGGYKSSFKOAKMMIRPKNFKP	432
Db	289	-----HGWWYSLKSVYMKIRNDEIP	309

```

RESULT      5
A38463
fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
C:Accession: A38463
R:Weisbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A:title: The beta chain of chicken fibrinogen contains an atypical thrombin
A:reference number: A38463; PMID:91182745
A:Accession: A38463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEI>
A:Cross-references: GB:MS8514; NID:g211779; PIDN:AAA48770.1; PID:g211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrin
F/373-20/Domain: fibrinogen disulfide ring homology <FDR>
F/212-460/Domain: fibrinogen beta/gamma homology <FEG>

```

Query Match	21.1%;	Score 493.5;	DB 2;	Length 463;
Best Local Similarity	30.4%;	Pred. No. 8.9e-28;		
Matches 137;	Conservative 58;	Mismatches 162;	Indels 93;	Gaps

QY	30	EDASAQAACPARLEGSGRCE-----GSOCFQQLTLPITLIQLPQLGSMEVLEKVRTL	83
DB	51	QDQAKMKGPPIIYDAGGCKHPDELUGVLCPTGCELOT-----TLLKOEKTV	97
QY	84	KEAVDSLKSCQCKIQADHRDPGCGNGGCAETABDSRVQELSSQVNLKSELKNAKDQ	143
DB	98	KPVLRLDK-----DRVAKFSD-----TSTMYQIVNMIDNKLKYTKQQRKDN	139
QY	144	---IOGLGRLETPHLVNNMNTIENYVDNKVANLTVVVNSLDGCKSCPSQBHMQSQ----	196
DB	140	DIILSEYNTEMELHYNYIKDNLDMNTIPSSLRLVRAVIDSLHKKIOKLENAIATQTDYCRS	199
QY	197	-----PVOHLLIYKDCSDHYVLGRSSGARVTPDHRNSSFEVYVCWETMGGGWTVLQ	248
DB	200	PCVASCNIPV--VSGRECEDIYRKGETSEMVIIDPPTTPYRYVCOMETDNGWTLIQ	257
QY	249	ARLDGSTNTREWKDYKAGFGNLER-----EFWLGNDKIHLLTKKEMILRLD	297
DB	258	NRODGSVNEGRAWDEYKRGFGNIASKGGKKYCDTPCEYWLGNDKISQLTKIGPTKVLLEM	317
QY	298	EDPNGULTYALYDOQFYVANEFLKYRLUHIQNYNGTAGDAUR--FSRHYN-----HDLRF	348
DB	318	EDNNGDKVSALYGGFTIHNEGNNKYOLSVSNYKGNAGNALMEGASOLYGENMTMTIHNGWY	377

```

QY   349 FTTDRNDRY-----PSGNCGLYTSYGWGFSCLSANLNGKY-----HOKYKGVNRG 397
      I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I :
Db    378 FSTYDRNDGWLTTPRKCQSKEDGGGWYNRC HAANPNRGYYWGTTYSDMAKHGTDDG 437

QY   398 IFWGTWPQINQAQGGGYKSFKQAKMMTRP 427
      I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I :
Db    438 IVWNWRKG-----SWY--SMKKMSMKIKP 459


RESULT 6
FGHUG
fibrinogen gamma-A chain precursor - human
N;Alternate names: coagulation factor I
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 25-Feb-1985 #text_change 21-Jul-2000
C;Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125;
R;Chung, D.W.; Chan, W.Y.; Davie, E.W.
Biochemistry 22, 3250-3256, 1983
A;Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma
A;Accession number: A90470; MUID:83283434
A;Accession: A90470
A;Molecule type: mRNA
A;Residues: 1-437 <CHU>
R;Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A;Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A;Reference number: A90494; MUID:85252774
A;Accession: B90494
A;Molecule type: DNA
A;Residues: 1-113,'I','I',115-437 <RIX>
A;Cross-references: GB:X02415; GB:M10014; NID:g182438; PIDN:AAB59531.1; PID:g182439
R;Henschel, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
In Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56,
A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
A;Reference number: A94433
A;Accession: C94433
A;Molecule type: protein
A;Residues: 27-437 <HEN>
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains:
A;Reference number: A93956; MUID:83247396
A;Accession: B93956
A;Molecule type: mRNA
A;Residues: 276-437 <KAN>
R;Porcace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A;Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t
A;Reference number: A92448; MUID:85030379
A;Accession: B92448
A;Molecule type: DNA
A;Residues: 286-437 <FOR>
R;Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A;Title: Isolation and characterisation of cDNA clones for the Alpha- and gamma-chain
A;Reference number: I37393; MUID:84069777
A;Accession: I37393
A;Status: preliminary; translated from GB/EMBL/DDDBJ
A;Molecule type: mRNA
A;Residues: 209-270 <RES>
A;Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:g577055
R;Bertagnoli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A;Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with
A;Reference number: A40698; MUID:93286185
A;Accession: A40698
A;Molecule type: protein
A;Residues: 27-33,'XX','XX',36-41 <BER>
A;Experimental source: thrombin-activated platelets
A;Note: Sequence extracted from NCBI backbone (NCBIP:133734)
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Trotter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994

```

A; residues. 27-33, AA 750-41 (BEN)
A; Experimental source: thrombin-activated platelets
A; Note: sequence extracted from NCBI backbone (NCBI
R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter,
Biochemistry 33, 1988-1993, 1994

[illegible]

```

101 KP-----NMIDAAFLKGRKMLE-EIMKYEASIIHTDSSIRYLQ-----EIYNSNN-----14
QY 166 VDNKVAFLTIVVNSLDGCKSKCPQSOEHMQSOPVOHLLYKDCSDHYVLGRSSGAYRVTDP 225
Db 145 --QKIVNLKPKVALEAQCE-PCKDPIVQ---IHDITGCKDCODIANKGAKOSGLYFIKPL 198
QY 226 HRNSSFEVYCDMETMGGWTVLQARLDGSGNTFTREWKDYKAGFNLN-----REFWLGNDK 281
Db 199 KANQOFLVYCEIDSGNGWTVFQKRLDGSVDKFNWIIQYKEGFGHLSPGTGTTFEWLGNEK 258
QY 282 IHLITKSKEM--ILRIDLEPNGLTYALYDQFVYANEFILYRLHIGNY-NGTAGDAL-- 336
Db 259 IHLISTOSAPYALRYVLEEDPNWGTSTADYAMFKVGPEDAKYRLTYAYFAGGDAGDAFDG 318
QY 337 -----RFSRHYNHDLRFFTPDRDNDRYPSGNGCLYVSSGWFDFDCLSANLNGKY 387
Db 319 FDFGDDPSDFE--FTSHNGWQFSTWMDNDKF-EGNCAEODGSGWNNKCHAGHLNGVY 375
QY 388 H-----QKYKGYVRNGIFWGTWPGINQAOPGGYK---SFKQAKMMIRPKN 429
Db 376 QGGTYSKASTPNGVDNGIIWATW-----KTRWYSMKKTTMKIIIPFN 416

RESULT 8
A25052
N:Contains: fibrinogen beta chain - sea lamprey (fragments)
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C:Accession: A25052; A03124; B03124
R:Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A:Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A:Reference number: A25052; MUID:87076582
A:Accession: A25052
A:Molecule type: mRNA
A:Residues: 39-479 <BOH>
A:Cross-references: GB:M14773; NID:g213191; PIDN:AAA49261.1; PID:g213192
R:Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A:Title: Amino acid sequences of lamprey fibrinopeptides A and B and charac
A:Reference number: A03120; MUID:77065679
A:Accession: A03124
A:Molecule type: protein
A:Residues: 1-36 <COT1>
A:Accession: B03124
A:Molecule type: protein
A:Residues: 37-42 <COT2>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibr
F:1-36/product: fibrinopeptide B #status experimental <PPB>
F:37-479/product: fibrin beta chain #status experimental <MAT>
F:90-217/Domain: fibrinogen disulfide ring homology <FDR>
F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
F:27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.1%; Score 470.5; DB 2: Length 479;
Best Local Similarity 30.5%; Pred. No. 4.1e-26;
Matches 133; Conservative 65; Mismatches 161; Indels 77; Gaps

QY 39 PARLEGGRCGEGSQCPQLTPLTTLIOLPRLGSMEEVLKEVTRLEAVDSLKKSQCQCK 98
Db 73 PQBAQKAIRDEGG-C--MLPESDLGVLCPGCELRBEILLKQRPDVRYKISMUKQNLYTYPI 129
QY 99 LQADHRRDPGGNGGAETAEDS-----RVQELSESQVNLSSLKLNKAQIOGLQGRLETF 153
Db 130 NSFD-----RMASDNTLKNQVOTLRRRLNRSSTHVAQKEI---ENRYKE 173
QY 154 LHLVNMNNIENYVDNKVANVTVVVNSLDGCKSK-----CPSQEHMQSQ-----VOHLLY 203
Db 174 VKI-----RIESTVAGSLRSMKSVLEHLRAKQMRBEAIAIKTKELCSAPCTVNCRPVPSG 229

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QY 361  SGNCGLYTSSG---WFFDSDCLSLANLNGKYIHQKTKYGVNRGIFWGTWPGINAOAPGGTKSS 41
Db 221  SINCASHSSYGRGAWWYKSCLLSLNLNGQYY--DYSGAPSY-IWYSYLPGDNDQIP----- 271

QY 418  FKQAKMMIR 426
      I : I : I
Db 272  FAEMKLRNR 280

RESULT 11
JC5980
      ficolin-A precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 18-Feb-2000
C:Accession: JC5980
R:Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachibana, Y.; Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A:Title: Molecular cloning and characterization of mouse ficolin-A.
A:Reference number: JC5980; MUID:98205801
A:Accession: JC5980
A:Molecule type: mRNA
A:Residues: 1-334 <FUJ>
A:Cross-references: DDBJ:AB007813; NID:g2957011; PIDN:BAA25126.1; PID:d1021021
A:Experimental source: liver
C:Comment: This protein consists of both collagen- and fibrinogen-like domains.
F:1-21/Domain: signal sequence #status predicted <SIG>
F:50-64, 68-106/Domain: collagen-like #status predicted <COL>
F:123-334/Domain: fibrinogen beta/gamma homology <FBG>

```

Query Match 19.8%; Score 463; DB 2; Length 334;
Best Local Similarity 44.0%; Pred. No. 8.8e-26;
Matches 99; Conservative 30; Mismatches 78; Indels 18; Gaps 7;

QY 204 KDCSDHYVLGRSSGAYRV--TPDHRNSSFEYYCDMETMGGTWTVLQARLDGSTNFTREWK 262
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 RSKCKDLLTRGIFLTGTWYTIHLPCR--PLATVLCMDVDVGSGTWTFORRYDGSIDFFRDWD 181
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 DYKAGFGNLEREPWLGNDKTHLLTKSEMLIRIDLEDENGLTLALYLYDOFYVANEFKYR 322
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 SYKRGFGNLCTEFLWLNNDYLHLLTANGNQELRVLDQDGKGSYAKYSFQVSEEQEYK 241
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 323 LHIGNY-NCTAGDALRFSRHYNHDLRFTPTDRDNDRYPSCNGLYISGWGFDSCLSAN 381
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 LTLQGLECTAGDSL--TKHNNS--FTTHDQNDA-NSMCAALFHGAWWYHNCQS 295
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 382 LNKYYHQYKGYRNGIFWGVTWPGINAOPOGKYKSSFQAOKMMIR 426
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 296 LNRYLGSSESADGINNCTGO-----GHHSYKVAEMKIR 332
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12

PGHUB

fibrinogen beta chain precursor - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C:Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121; A37
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; MUID:91344740
A:Accession: B43568
A:Molecule type: DNA
A:Residues: 9-191,'P',193-491 <CHU>
R:Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A:Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribon
A:Reference number: A90469; MUID:83283433
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CH1>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191,'A',193-491 <CH2>
A:CROSS-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R:Huber, P.; Dalmon, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A:Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A:Reference number: I37389; MUID:87146483
A:Accession: I37389
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:CROSS-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R:Henschel, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A94433
A:Contents: carbohydrate binding
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137,'QS',140-144,'QF',147-491 <HEN>
R:Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; MUID:79124640
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144,'QF',147-231,'D',233-330,'E',332-491 <WAT>
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976

A:Residues: 1-21 <SU>
 R:Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A:Reference number: A37507; MUID:79164394
 A:Accession: B37507
 A:Molecule type: protein
 A:Residues: 22-53 <MR>

Db	220	KIIRNEGTTSEMYLIQPEDSSKPYRVYCDMKTKEGGTWTIQNRQDGSGLDFGRKWDPKYG	279
Qy	268	FGNLER-----EWLGNDKTHLLTKSKEMILRLDLEDFENCLTLIALYDOFYVA	315
Db	280	FGNLTATNAEGKKYCGVPEYWLGNDRISQLTNMGPTKLLIEMEDGDKGKVATLYEGFTVQ	339
Qy	316	NEFLYRLHIGNYNGTAGD-----RFSRHYNHDLRFETTPORDNDRY-----PSG	362
Db	340	NEANKYQLSVYSYKGTAGNALLBCASOLVGENRTWTIHSWFSTYTDNRDNGKWTDPKR	399
Qy	363	NCGLYYSGWFWDFCLSANLNGKY-----HOKYKGVNRGIFWGTWPGINOAQPGYK	415
Db	400	QCSREDGGWYNYRCHAANNGRYWGGATYDMDAKHGCTDDGVVWNNWG-----SWT-	452

JU06/73
 restrictin precursor - chicken
 C.Species: Gallus gallus (chicken)
 C.Date: 10-Sep-1999 #sequence:rev1
 C.Accession: J01675; PS0385; S2325
 R.Noerenberg, U.; Wille, H.; Wolff
 Neuron 8, 849-863, 1992
 A.Title: The chicken neural extrac

A:Reference number: JH0675; MUID:92265298
A:Accession: JH0675
A:Molecule type: mRNA
A:Residues: 1-1353 <NOE>
A:Cross-references: GB:X64649; NID:g63613; PIDN:CAA45920.1; PID:g63614
A:Experimental source: brain
A:Accession: PS0385
A:Molecule type: protein
A:Residues: 579-586;827-840 <NOE1>
C:Comment: This protein is a neural extracellular matrix protein implicated in neural cell adhesion.
C:Superfamily: restrictin; fibrinogen beta/gamma homology; fibrinogen type I
C:Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycoprotein
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-1353/Product: restrictin #status predicted <MAT>
F:234-229/Domain: EGF homology <EG1>
F:265-291/Domain: EGF homology <EG2>
F:296-322/Domain: EGF homology <EG3>
F:324-405/Domain: fibrinogen type III repeat homology <EG4>
F:413-494/Domain: fibrinogen type III repeat homology <FN2>
F:502-584/Domain: fibrinogen type III repeat homology <FN3>
F:592-676/Domain: fibrinogen type III repeat homology <FN4>
F:684-764/Domain: fibrinogen type III repeat homology <FN5>
F:772-853/Domain: fibrinogen type III repeat homology <FN6>
F:861-941/Domain: fibrinogen type III repeat homology <FN7>
F:949-1027/Domain: fibrinogen type III repeat homology <FN8>
F:1035-1115/Domain: fibrinogen type III repeat homology <FN9>
F:1130-1338/Domain: fibrinogen beta/gamma homology <FBG>
F:1272-1286/Region: calcium binding #status predicted
F:53,197,277,391,469,580,734,790,960,1031,1041,1256,1342/Binding site: carbohydrate (Asn)

Query Match 19.4%; Score 454.5; DB 1; Length 1353;
Best Local Similarity 41.0%; Pred. No. 2.1e-24;
Matches 94; Conservative 33; Mismatches 83; Indels 19; Gaps 6;

Qy 204 KCSRDHYLVGRSSGAYRTPD-HRNSFFVYCDMETGGWTVLQRLDGTFTREWK 262
Db 1131 DKAQHLMGNDTLGGVYTSINGDLSQVQVFCDMSTDGGWIVFORRQGLTDFRKWA 1190
Qy 263 DYKAGGFLNERFWLGNKTHLLTKSKEMTLRLDLEDFNLTYALYDQFVANEFLKYR 322
Db 1191 DYRVGFNLDEFEWGLDNLHKITSQGRYELDMRD-GOEAAVAYYDKFSGVDSRSLYK 1249
Qy 323 LHIGTNGTAGDALRSRHHYHDLRFTPTDRNDRYPSGNGLYSSGWWFDSCLSNL 382
Db 1250 LRIGDTNGTSGDSLTY-----HGRPFSTKDRND-VAVTNCAMSYKGAWWYKNCCHRTNL 1303
Qy 383 NGKYHOKYKGVNRGIFWGTWPGINOAQPGYKSSFKQAKMIRPKNFK 431
Db 1304 NGKYGESRHS--QGINWYHWK-----GHEFSIPFVEMKMRPNYHR 1341

RESULT 15
D44234
fibrinogen alpha chain precursor, extended splice form - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide A
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
C:Accession: D44234; B44234
R:Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redman
Biochemistry 31, 11968-11972, 1992
A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
A:Reference number: A44234; MUID:93090725
A:Accession: D44234
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA; DNA
A:Residues: 1-866 <FUI>
A:Cross-references: GB:M58569; NID:gl82406; PID:g182407
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
A:Accession: B44234
A:Molecule type: mRNA; DNA

A:Residues: 605-866 <FU2>
A:Note: sequence extracted from NCBI backbone (NCBIP:119917)
C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleav
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics: See PIR:FGHUA for the major splice form. It is not known whether this form
C:Genetics:
A:Gene: GDB:FGA
A:Cross-references: GDB:119129; OMIM:134820
A:Map position: 4q28-4q28
A:Introns: 18/3; 60/3; 122/1; 171/2
A:Note: the list of introns is incomplete
C:Complex: The fibrinogen molecule is a hexamer containing two sets of three nonident
ntained in the core. Two three-chain coiled coils emerge from this core and connect i
distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
C:Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprot
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <APT>
F:36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F:57-185/Domain: fibrinogen disulfide ring homology <DR>
F:591-593/Region: cell attachment (R-G-D) motif
F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
F:22,460/Binding site: phosphate (Ser) (covalent) #status experimental
F:35-36/Cleaveage site: Arg-Gly (thrombin) #status experimental
F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
F:55/Disulfide bonds: interchain (to beta-95) #status experimental
F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
F:68/Disulfide bonds: interchain (to beta-106) #status experimental
F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
F:184/Disulfide bonds: interchain (to beta-223) #status experimental
F:288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F:322/Cross-link: isopeptide (Lys) (interchain to alpha-2-plasmin inhibitor 41-Gln) #
F:347,385/Cross-link: isopeptide (Gln) (interchain to alpha) #status experimental
F:461-491/Disulfide bonds: #status experimental
F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to alpha) #status pred
F:686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 454; DB 2; Length 866;
Best Local Similarity 39.4%; Pred. No. 1.3e-24;
Matches 102; Conservative 41; Mismatches 74; Indels 42; Gaps 11;

Qy 192 HMQSOPVOHLIYKDCSDHYVL-----GRRSSGAYRTPDHRNSSFFVYCDMETGGWTVL 247
Db 623 HAKSRPV-----RDCDD--VLQTHPSGTQSGIFNKLPGSSKIFSVYCDQETSLGGWLLI 675
Qy 248 QARLDGSTNFTREWKYKAGFNL-----ERFEWGLNDKTHLLTKSKEMTLRLDLEDFNGL 303
Db 676 QQRMDGSLNFNTWQDYKRGFGSLNDEGEFGLWGLNDYLLHLTQ-RGSVLRVELDEWAGN 734
Qy 304 TLAYLDQFYVANEFLKYRLHIGTNGTAGDAL-----RFSRHHYHDLRFTFTDPRND 357
Db 735 EAYAEY-HFRVSEAEGLALQVSSVEGTAGDALIEGSEVEGAFTSHNNQFSTFDRDAD 793
Qy 358 RYPSGNCGLIYSSGWWFDSCLSANLNGKY-----HOKYKGVNRGIFWGTWPGINQ 408
Db 794 QWEE-NCAEVYGGGWWYNNCOAANLNGIYYPGGSYDPRNNSPYE-IEGCVVWVSFRGADY 851
Qy 409 AOPGGYKSSFKQAKMIRP 427
Db 852 -----SLRAVRMKIRP 862

Search completed: February 27, 2001, 12:50:13

Job time: 157 sec

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:48:38 ; Search time 30.15 Seconds
(without alignments)
489.941 Million cell updates/sec

Title: US-09-442-143-4

Perfect score: 2340

Sequence: 1 MRLPGWLSSAVLAACRAV.....GYKSSFKQAKMIRPKFKP 432

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq/AA1991.DAT:*
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14: /SIDS1/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq/AA1995.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2340	100.0	432	W88236	Mouse prothrombina
2	1853.5	79.2	439	W88235	Human prothrombina
3	537.5	23.0	499	W47529	Amino acid sequenc
4	533.5	22.8	314	R65759	Rat hepatic parench
5	533.5	22.8	496	W01411	Human TIE-2 ligand
6	533.5	22.8	496	R94605	Human TIE-2 ligand
7	533.5	22.8	496	W47532	Human TIE-2 ligand
8	533.5	22.8	496	W47532	Human angiotensin
9	533.5	22.8	496	W47532	Human angiotensin
10	528	22.6	498	W47528	Amino acid sequenc
11	524	22.4	312	R94317	Hepatocyte prolif
12	522	22.3	312	R94316	Hepatocyte prolif

13	521	22.3	312	15	R65760	Human hepatic pare
14	507	21.7	346	20	Y23736	Human AR-1 protein
15	507	21.7	346	20	Y05399	Human TIE ligand N
16	494.5	21.1	461	21	Y66727	Membrane-bound pro
17	494.5	21.1	496	19	W47527	Amino acid sequenc
18	493	21.1	495	21	Y78904	Angiotensin fusio
19	490	21.1	495	21	Y78907	Angiotensin fusio
20	490	20.9	494	19	W47526	Amino acid sequenc
21	489.5	20.9	497	17	W01410	Human TIE-2 ligand
22	489.5	20.9	497	17	R94604	Human TIE-2 ligand
23	489.5	20.9	497	19	W47531	Amino acid sequenc
24	489	20.9	498	17	W01409	Human TIE-2 ligand
25	489	20.9	498	17	R94603	Human TIE-2 ligand
26	489	20.9	498	19	W47530	Amino acid sequenc
27	489	20.9	498	21	Y78902	Human angiotensin
28	489	20.9	498	21	Y78905	Human angiotensin
29	488.5	20.9	453	16	R82245	Human fibrinogen g
30	488.5	20.9	453	16	R82246	Human fibrinogen g
31	488	20.9	491	20	Y26196	Human zapo3 protei
32	488	20.9	491	20	Y05397	Human TIE ligand N
33	488	20.9	491	21	Y69483	Amino acid sequenc
34	488	20.9	491	21	Y68761	An angiotensin-re
35	483.5	20.7	493	20	Y05396	Human TIE ligand N
36	483.5	20.7	493	21	Y70745	PSEQ-3 protein enc
37	483.5	20.7	493	21	Y54999	Human scarface 1 p
38	483	20.6	491	21	Y44841	Human secreted pro
39	480.5	20.5	411	16	R84650	Fibrinogen gamma c
40	476.5	20.4	509	19	W47533	Amino acid sequenc
41	474.5	20.3	509	19	W26792	Mouse TIE-2 recept
42	470	20.1	503	19	W47534	Amino acid sequenc
43	470	20.1	503	19	W26791	Human TIE-2 recept
44	470	20.1	503	20	Y23735	TIE ligand-4 (TL4)
45	465.5	19.9	454	16	R84551	Partial human fibr

ALIGNMENTS

RESULT 1

W88236
ID W88236 standard; Protein; 432 AA.

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DT 15-MAR-1999 (first entry)

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applicant

Mouse prothrombinase Fg12 protein.

Prothrombinase; Fg12; mouse; immune coagulation; antibody;
inhibitor; infection; graft rejection; glomerulonephritis; cancer;
gastrointestinal disease; foetal loss; therapy; vaccine.

Mus sp.

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Location/Qualifiers
172..174

/label= Asn is N-glycosylated

228..231

/note= "Asn is N-glycosylated"

256..259

/note= "Asn is N-glycosylated"

323..325

/note= "Asn is N-glycosylated"

213..439

/note= "fibrinogen related domain"

WO9851335-A1.

19-NOV-1998.

15-MAY-1998;

98WO-CA00475.

10-OCT-1997;

97US-0061684.


```

Db 1 mklanywylssavlatyglvlnaneteeikderakdvprlesrgkceagecpgvs 60
QY 59 LPTLTQLPRLQSGMEVLEKVRTLKAVDSLKSCODCKLQADDDHDPGGNG---GNG 114
Db 61 lplltlqlpkqfrievefkeqnlkeivnsllkscqcklqadddgprngllpstdg 120
QY 115 AE-TAEDSRVQLESQVNLSSSELKNAKQIQGLQGRLETLHLVNMNNIENYDNKVANL 173
Db 121 apgevgnrvrelesevnklsselknakeeinvlghrlekinlvnmnnienyvdskvanl 180
QY 174 TVVNSLDGCKSCPKQEHMQSPVQHLYKDCSDHYVLGRRSSGAYRVTPDHRNSSFEV 233
Db 181 tfvnsldgckscpsqegqlsqrpvghlykdcsvyagkrsetyrvtpdpknssfev 240
QY 234 YCDMETMGSGWTVLQARLDGSTNFTREWKDYKAGFGNLEREFWLGNDKIHLLTKSEKIL 293
Db 241 ycdmetcmg99wtvlgarldgstnftwqdykagfgnlrrefwlgndkhlhlltksemil 300
QY 294 RIDLEDFNLITLYALYDQFYVANEFLKYLRLHIGNYNGTAGDALRFSRHYNHDLRFFTTPD 353
Db 301 ridledfngvelyaldyqfyvaneflikylrhvngnyngtagdalrnfkhnhdklfttpd 360
QY 354 RONDYPSGNGLYYSSGWNWFDSCLSANLNGKYYHOKYKGVNRGIFWGTWPGINQAOPGG 413
Db 361 knddrypsngcglyssgwwfdacslanlngkyyhkyrgvrngifwgtwpgvseahpgg 420
QY 414 YKSSFKQAQMMIRPKNFKP 432
Db 421 ykssfkqaqmmirpkhfkp 439

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RESULT 3

W47529
ID W47529 standard; Protein; 499 AA.

XX AC W47529;

XX DT 09-SEP-1998 (first entry)

XX DE Amino acid sequence of chimeric TIE ligand IN2C2F (chimera 3).

XX KW Chimeric TIE ligand IN2C2F; TIE-2 ligand; neovascularisation; tumour; human.

XX OS Homo sapiens.

XX PN WO9805779-Al.

XX PD 12-FEB-1998.

XX PF 01-AUG-1997; 97WO-US13557.

XX PR 25-OCT-1996; 96US-0740223.

XX PR 02-AUG-1996; 96US-0022999.

XX PA (REGE-) REGENERON PHARM INC.

XX PI Davis S, Yancopoulos GD;

XX DR WPI; 1998-145615/13.

XX DR N-PSDB; V18616.

XX PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound healing

XX PS Claim 20; Fig 26; 202pp; English.

XX CC This is the amino acid sequence of the chimeric TIE ligand IN2C2F, used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host cells used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are

CC useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing the TIE receptor and for attenuating or preventing tumour growth in a human.

XX SQ Sequence 499 AA;

Query Match 23.0%; Score 537.5; DB 19; Length 499;
Best Local Similarity 28.4%; Pred. No. 2.2e-39;
Matches 149; Conservative 83; Mismatches 165; Indels 127; Gaps 19;

```

Qy 7 LWLSSAVLAACRAVEEHNLTEGLEDAQAACPARLEGSG---RCEGSCQCPQLTLP-- 60
Db 3 vflsfafiala-----lth--icgcnqrsp---ensgrrynriqhgqccaytilpsh 50
Qy 61 -----TTLTIQLPRLQSGMEVLEKVRTLKEAV-----DSLKK 92
Db 51 dgcncresttdgynntalqrdaphvdpddsvqlrvlenlmenntqwlmklenyiqdnmkk 110
Qy 93 SCQDCKLQADDDR-----DPGGNGNGAETAEDSR-VQELSEQV----- 130
Db 111 emveiqgnavqngqtavmieigtlnln--qtaeqtrkltdveagvlnqtrtleqllehs 168
Qy 131 --NKLSSSELKNAKQIQGLQGR-----LETLHLVNMNNIENYVDN---KVALTV 175
Db 169 stnklekqildqtseinklqdknsflekkvamedkhhiiqisikeekdqlqvlvskqns 228
Qy 176 VVNSLDGKC-----SKPQSEHMQSQPVQHLLI-----YKDCS 207
Db 229 lilelekkivtatvnnsvlqkqhdmetvnnlltmmstnsakdptvakeeqisfrdca 288
Qy 208 DHYVILGRRSSGAYRVTPDHRNSSFEYCDMETMGSGWTVLQARLDGSTNFTREWKDYKAG 267
Db 289 evfksghntnglytlitfpnsteeikaycdmeaggvgwtliqrredgsvdqfgrtkeykvg 348
Qy 268 FGNLEREFWLGNDKIHLLTKSEKILRIDLEDFNLITLYALYDQFYVANEFLKYLRLHIGN 327
Db 349 fgnpsgeyglnefvsqitngqrvyvikhlkdwegneayslyehfysseelnryrlhkg 408
Qy 328 YNGTAGDALRFSRHYNHDLRFFTTPDNDYPSGNGLYYSSGWNWFDSCLSANLNGKYY 387
Db 409 ltgtagkissisqpgnd----fstkdgndkcic-kcsqmltggvwwfdacgspnngmyy 463
Qy 388 HQYKGVPR-NGIFWGTWPGINQAOPGGYKSSFKQAQMMIRPKNF 430
Db 464 pqrqntnknfngikwywkg-----sgy--slkattmmirpadf 499

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RESULT 4

R65759
ID R65759 standard; protein; 314 AA.

XX AC R65759;

XX DT 17-MAY-1995 (first entry)

XX DE Rat hepatic parenchymal cell growth factor.

XX KW Hepatic parenchymal cell growth factor; HPGF; liver diseases; liver cancer; cirrhosis.

XX OS Rattus rattus.

XX FH Key Location/Qualifiers

XX FT Peptide 1..24

XX FT /label= sig_peptide

XX PN WO9421678-A.

XX PD 29-SEP-1994.


```

AC R94605;
XX
DT 28-OCT-1996 (first entry)
XX
DE Human TIE-2 ligand 2 derived from pBluescript KS clone.
XX
KW Angiogenesis; neovascularisation; tumour development; wound healing;
KW TIE; tyrosine kinase with Ig and EGF homology domains; vector;
KW recombinant; clone; diagnosis; ischaemia; thromboembolytic disease;
KW atherosclerosis; inflammation; diabetes; ligand bodies; delivery;
KW targeting.
XX
OS Homo sapiens.
XX
PN WO9611269-A2.
XX
PD 18-APR-1996.
XX
PF 06-OCT-1995; 95WO-US12935.
XX
PR 06-APR-1995; 95US-0418595.
PR 07-OCT-1994; 94US-0319932.
PR 27-OCT-1994; 94US-0330261.
PR 02-DEC-1994; 94US-0348492.
PR 09-DEC-1994; 94US-0353503.
PR 17-JAN-1995; 95US-0373579.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Aldrich TH, Bruno J, Davis S, Goldfarb M, Jones PF;
PI Maisonnier PC, Radziejewski C, Yancopoulos GD;
XX
DR WPI; 1996-209850/21.
DR N-PSDB; T14650.
XX
XX
PT Nucleic acid encoding TIE-2 ligand and related vectors - useful in
PT diagnosis and treatment of neovascularisation, tumours, etc., or to
PT promote wound healing, etc.
XX
XX
PS Claim 2; Fig 6; 84pp; English.
XX
CC R94605 is a human TIE-2 (hTIE-2) ligand 2 derived from a pBluescript
CC KS clone. hTIE-2 ligand DNAs of the invention are recombinant versions
CC of the native ligand coding sequences and may be used to produce the
CC ligands at a high yield. Antibodies and receptor bodies that bind to
CC TIE-2 ligands may be used to inhibit angiogenesis and neovascularisation
CC (e.g. associated with tumour development) and the TIE-2 ligands
CC themselves are useful to promote neovascularisation and wound healing
CC e.g. for treatment of ischaemia. TIE-2 ligands are also useful to
CC treat thromboembolytic disease, atherosclerosis, inflammation and
CC diabetes. Ligand bodies contg. TIE-2 ligands may also be useful for
CC the delivery and targeting of growth factors, toxins etc. to sites
CC where their presence is advantageous.
XX
SQ Sequence 496 AA;

Query Match 22.8%; Score 533.5; DB 17; Length 496;
Best Local Similarity 29.4%; Pred. No. 4.9e-39;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CPGSQCPF-----QLTLPRLTTLQPLQSGMEVLKE---VPTLKEAV-DSLKKSCQDC 97
Db 53 crsspsvsnvraqdpleyddsqrqlrvlenimntqwmklnyiqdmkkmvei 112
QY 98 KIQADDDR-----DPGGNGNGAETAEDGR-VOELSQV-----NKL 133
Db 113 qnavnqtavmieglthlln--qtaetrktdvcaqlnqttrlelqllehlstnkl 170
QY 134 SSELNKAQDIQGLQGR-----LETLHLVNNNIENYVDN---KYANLTVVVNSL 180
Db 171 ekqildqtseInkldqnsflekvlamedkhiqisikeekdqqlvlskqnsiieel 230

181 DKC-----SKPSEQHMQSQPVQHLI-----YKDCSDHYVL 212
231 ekkiatvtnnsvlqkqghdmetvnnlltmnstsnsakdptvakeeqisfrdcaevfks 290
QY 213 GRRSSGAYRVPDHRNSSFEVYCDMETGGGHTVLQARLDGSTNFTREKDKYKAGFGNLE 272
Db 291 ghtnglyltlfpnsteeikaycdmeagggwtliqrrredgsdvtqrkweykvqfgnps 350
QY 273 REFVLGNDKIHLLTKSKEMILRIDLEDFENGLTLYALYDQFYVANEFLKYLRLHIGNYNGTA 332
Db 351 geywlgnefvsqltnqqrvihihkdwegneaylyehfyisseelnyrihlkgtlgtga 410
QY 333 GDALFRSHYNHDLRFFTPDRDNDRYPFSGNGLYSSGWDFDCLSANLNGKYHQQYK 392
Db 411 gkissisqpgnd----fstkgdndkcic-kcsqmltggwdfdacgpnolngmyypqtn 465
QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKQAKMMIRPKNF 430
Db 466 tnkfnglkwywvkg-----sgy--slkattmmirpadf 496

RESULT 7
W47532
ID W47532 standard; Protein; 496 AA.
XX
AC W47532;
XX
DT 09-SEP-1998 (first entry)
XX
DE Human TIE-2 ligand 2 from clone pBluescript KS.
XX
KW Chimeric TIE ligand 2N1CLF; TIE-2 ligand; neovascularisation;
KW tumour; human.
XX
OS Homo sapiens.
XX
PN WO9805779-AL.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13557.
XX
PR 25-OCT-1996; 96US-0740223.
PR 02-AUG-1996; 96US-0022999.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Yancopoulos GD;
XX
DR WPI; 1998-145615/13.
DR N-PSDB; V18619.
XX
PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing
XX
XX
PS Example 8; Fig 6; 202pp; English.
XX
CC This is the amino acid sequence of the human TIE-2 ligand 2,
CC used in the method of the invention, involving the production
CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
CC and host cells used in the method of the invention are useful for
CC the recombinant production of the ligands. The ligands, etc. are
CC useful for blocking blood vessel growth, promoting neovascularisation,
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.
XX
SQ Sequence 496 AA;

Query Match 22.8%; Score 533.5; DB 19; Length 496;
Best Local Similarity 29.4%; Pred. No. 4.9e-39;

```


PN	WO200002584-A2.
XX	
XX	20-JAN-2000.
XX	
XX	12-JUL-1999; 99WO-US15600.
XX	
PR	13-JUL-1998; 98US-0092672.
PR	02-DEC-1998; 98US-0110608.
XX	
XX	(TEXA) UNIV TEXAS SYSTEM.
XX	
PI	Thorpe PE, Ran S;
XX	
DR	WPI; 2000-182175/16.
DR	N-PSDB; Z92215.
XX	
PT	New composition for killing tumour vascular endothelial cells for
PT	treating solid tumours, comprises unconjugated anti-aminophospholipid
PT	antibody -
XX	
PS	Disclosure; Page 223-224; 226pp; English.
XX	
CC	This sequence represents the human angiotensinogen-2 (Ang-2) amino acid
CC	sequence. Ang-2 is a naturally occurring angiogenesis antagonist when
CC	vascular endothelial growth factor (VEGF) levels are low, and generally
CC	counteracts the blood vessel maturation and stability mediated by Ang-1.
CC	Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation
CC	or stabilisation factor, converting immature vessels to mature vessels.
CC	Both Ang-1 and Ang-2 are useful in a therapeutic approach to the
CC	treatment of vascularised tumours. The invention relates to a composition
CC	comprising an anti-aminophospholipid antibody, or its antigen binding
CC	region. The composition is used to kill tumour vasculature endothelial
CC	cells. Aminophospholipids are stable and specific markers accessible on
CC	the luminal surface of tumour blood vessels. Ang-1 or Ang-2 may be used
CC	in the composition of the invention. The composition is used to treat
CC	malignant or benign vascularised tumours in animals, especially large
CC	tumours.
XX	
SQ	Sequence 496 AA; SQ

Query Match	22.8%; Score 533.5; DB 21; Length 496;
Best Local Similarity	29.4%; Pred. No. 4.9e-39;
Matches 135; Conservative	80; Mismatches 153; Indels 91; Gaps 16;
QY	48 CEGSOCP-----OLTPTLTIQLPROLGSMEEVLKE----VRTLUKAV-DSLKKSCODC 97 : : : : : : : : : : : : : : : : : : : :
Db	53 crssspysnavrdapleyddsvgrlqvlenimentqwlmkienyiqdmnkkmvei 112 : : : : : : : : : : : : : : : : : : : :
QY	98 KIQADDHR-----DPGGNGGNAETADSR-VQELESQV-----NKL 133 : : : : : : : : : : : : : : : : : : : : : : : :
Db	113 qqnavaqnvqtavmieigtnalln--gtaeqrkltdveaqvlnqgtrtleqllehsistnkl 170 : : : : : : : : : : : : : : : : : : : : : : : :
QY	134 SSELAKNAKDQIOGLGR-----LETUHLVNMMNIENVDN---KVANLTVVVNSL 180 : : : : : : : : : : : : : : : : : : : : : : : : :
Db	171 ekqlldtsetlnkldqknaflekklvamedkhilqliskekdqlvlvsqnsifeel 230 : : : : : : : : : : : : : : : : : : : : : : : :
QY	181 DGKC-----SKCPSQEHMQSQPVQHLLI-----YKDCSDHYVL 212 : : : : : : : : : : : : : : : : : : : : : : : :
Db	231 ekkivtatvnsvlqqkqhdlmetvnlltmstsnasakptvaekeeqisfrdcaevfks 290 : : : : : : : : : : : : : : : : : : : : : : : :
QY	213 GRRSSGARVTPDHRNSSFEVCWETMGGGWTVLOARLDGSTNFTREWKDYKAGFGNLE 272 : : : : : : : : : : : : : : : : : : : : : : : :
Db	291 ghtnglyltftpnsteekaycmeagggwtliqrredgsvdfeqrktwekykvfgnps 350 : : : : : : : : : : : : : : : : : : : : : : : :
QY	273 REFWLGNDKIHLLKREMILRIDLEFNGULTLYALYDQFVANEFYLRLHIGNYCTA 332 : : : : : : : : : : : : : : : : : : : : : : : :
Db	351 geywlgnefvsqltoqryrvlkhlkwedgneayslvehfylsseelnryihlkgltgta 410 : : : : : : : : : : : : : : : : : : : : : : : :
QY	333 GDALFRSHYNHDRFTPTPPDRNDPRPSGCGLYYSSGWWFDSCLSANLNKYYYHQKYK 392 : : : : : : : : : : : : : : : : : : : : : : : :
Db	411 gktissispqnd----fstkdgdndkcic-kcsqmltgawfdacgpnlnmqypqrqn 465 : : : : : : : : : : : : : : : : : : : : : : : :

```

Qy 393 GVR-NGIFWGPWPGINGAOPGGYKSSFPQAKMMIRPKNF 430
      : ||| | | | | | | | | | | | | | |
Db 466 tnkfngikwywkg-----sgy--slkattmmirpadf 496

RESULT 10
W47528
ID ID W47528 standard; Protein: 498 AA.
XX AC AC
XX AC AC
XX W47528;
XX
DT 09-SEP-1998 (first entry)
XX
DE Amino acid sequence of chimeric TIE ligand I1NC2F (chimera 1).
XX
KW Chimeric TIE ligand I1NC2F; TIE-2 ligand; neovascularisation;
KW tumour; human.
XX
XX Homo sapiens.
XX OS
XX PN W09805779-A1.
XX
XX PD 12-FEB-1998.
XX
XX PF 01-AUG-1997; 97WO-US13557.
XX
XX PR 25-OCT-1996; 96US-0740223.
XX PR 02-AUG-1996; 96US-0022999.
XX
XX PA (REGE-) REGENERON PHARM INC.
XX
XX PI Davis S, Yancopoulos GD;
XX
XX DR WPI: 1998-145615/13.
XX DR N-PSDB; V18615.
XX
XX PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
XX healing
XX
XX PS Claim 20; Fig 24; 202pp; English.
XX
CC This is the amino acid sequence of the chimeric TIE ligand I1NC2F,
CC used in the method of the invention, involving the production
CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
CC and host cells used in the method of the invention are useful for
CC the recombinant production of the ligands. The ligands, etc. are
CC useful for blocking blood vessel growth, promoting neovascularisation
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.
XX
XX SQ Sequence 498 AA;

Query Match 22.6%; Score 528; DB 19; Length 498;
Best Local Similarity 31.8%; Pred. No. 1.5e-38;
Matches 140; Conservative 70; Mismatches 142; Indels 88; Gaps

Qy 19 AVEEHNL-----TEGLEDAQAACPARLEGSGRCGSGCPFPQLTPTL-TIQLPRQ-L 70
      ||: | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 avqhtatmteigtllsqtaeqtrktdvtetvqlngtsrleiglilenslstykiekql 178

Qy 71 GSMEEVLK--EVRTL-----KEAVDSLKKSQCDCKLQADHRDPGGNGNGAE 116
      ||: || | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 qqtneilkiheknsllhekilemegkhkeeldtikeeknlq-----giv 223

Qy 117 TAEDSRVQVELESQVKNLSSELKNAQDQIOGLOGRLETLH-LVNMMNIENYVDKNVANLTV 175
      | : : ||||| | | : : | | | : : || | | | | | | | | | | | |
Db 224 trqtyiqelqklnratt--nnsvlqkqgle-lmdtcvhnlnv----- 264

Qy 176 VVNSLDGCKSK----CPSQEHMQSQPVQHLLIYKCDSDHYVLGRSSGAYRVPTPDHRRNSF 231
      | : | : : | : : | : : | : : | : : | : : | : : | : : | : :

```

Query Match	22.6%	Score 528;	DB 19;	Length 498;
Best Local Similarity	31.8%	Pred. No. 1.5e-38;		
Matches 140; Conservative	70;	Mismatches 142;	Indels 88;	Gaps 17;

```
QY      19  AVEEHNL-----TEGLEDSAAQAACPARLEGSGRCGSCQPQLTLPTL-TIQLPRQ-L 70  
        ||: |   |   |   |   |   |   |   |   |   |   |   |   |   |  
Db     119  avqhtatmleigtllsqtaetrkltldvetylmgtsrleqlilenslstyklekqll 178  
  
QY      71  GSMEEVLIK-----KEAVDSLKRSQCQDKCQLQADHRDPGGNGCGAE 116  
        ||: |   |   |   |   |   |   |   |   |   |   |   |   |  
Db     179  qgtneilikheksnlltkhleemegkhkeeldtlkeekenlq-----gfv 223  
  
QY     117  TAEDSRVQELESQVNKLSELNAKDQIQLOGRLETLH-LVMNNNIENYVDNKVANLTV 175  
        |: |::|||: |: |: |   |   |   |   |   |   |   |   |   |  
Db    224  trtqiieklekqlnratt--nsrvlqkqqle-lmdtvhnlnvl----- 264  
  
QY     176  VWSNLDGCKSK----CPSEQHMOSQPQHLLIYKDCSDHYVLGRSSGAYRVTPDHRNSSF 231  
        |: |   |   |   |   |   |   |   |   |   |   |   |   |
```

```

Db 265 -----ctkegvllkkgkreekp-----frdcaevfksghttngiyltlfnpsteei 311
QY 232 EYVCDMETMGCGTWTVLQARLDGSTNFTREWKDYKAGFNGLEREFWLGNDKIHLLTKSKEM 291
:||||| |||||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 312 kaycdmeagggwtliqirredgsvdfrtkeykvfgnpsgeywlgnfsvqlnqgry 371
QY 292 ILRLDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRHHYHDLRFPTT 351
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 372 vlikhlkdwegneayslyedfylseeinyrihlkgltagklssisqpgnd-----fst 427
QY 352 PDRNDRYPSGNCGLIYSSGWFWFSCLSANLNGKYHOKYKGVN-NGIFWGTWPGINQAO 410
:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 428 kdgndkic-kcsqmitlgwfwfadcpsnlnngmypprqntknfnglkwywkg-----481
QY 411 PGGYKSSFKQAKMMIRPKNF 430
||| | |||||:|
Db 482 -sgy--slkattmirpadf 498

RESULT 11
R94317
ID R94317 standard; Protein; 312 AA.
AC R94317;
XX
XX
DT 05-NOV-1996 (first entry)
XX
DE Hepatocyte proliferation substance HP-041V.
XX
KW Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter;
KW chinese hamster ovary cell; CHO; hepatitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22 /note= "signal peptide"
FT Protein 23..312 /note= "mature protein"
XX
XX
PN WO9609383-A1.
XX
XX
PD 28-MAR-1996.
XX
XX
PF 21-SEP-1995; 95WO-JP01904.
XX
XX
PR 22-SEP-1994; 94JP-0228234.
XX
XX
PA (TAISHO ) TAISHO PHARM CO LTD.
XX
XX
PI Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;
XX
DR WPI; 1996-188445/19.
DR N-PSDB; T13397.
XX
XX
PT Vector for expression of hepatocyte proliferation substance - in
PT eukaryotic cells, used as diagnostic reagent for hepatitis and for
PT basic research on in vitro liver cell cultures
XX
PS Example 3; Page 28-29; 44pp; Japanese.
XX
CC This is the amino acid sequence of a variant human hepatocyte
CC proliferation substance (HPS). The variant differs from the sequence
CC encoded by T13396 at pos. 214: A to G change and pos. 314: T to C. These
CC changes alter the amino acid residues at pos. 50 of the mature protein:
CC Ile to Val and pos. 83: Leu to Pro. The gene was isolated from a
CC lambda-gt10 human cDNA library using the sequence T13396 as a probe.
CC The human gene was cloned in plasmid pSCL to produce plasmid pSVLH which
CC was subsequently recombined to produce plasmid pcdLH-dhfr in which the
CC HPS gene is under control of the SR-alpha promoter. This plasmid is
CC transformed into CHO cells to express the HPS protein. The HPS protein
CC can be used to diagnose hepatitis.
XX

```

```

SQ Sequence 312 AA;
Query Match 22.4%; Score 524; DB 17; Length 312;
Best Local Similarity 37.8%; Pred. No. 1.7e-38;
Matches 126; Conservative 41; Mismatches 114; Indels 52; Gaps 11;
QY 112 GNGAETAEDSRVQE--LESQVKNKLSSELAKNAKDQIOGLQGRLETLHLVNNNNIENYVDNK 169
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 17 greisaledcaeqemlraqvrlletrvk-----gqgvkikqllgenevq-fldkg 66
QY 170 VANLTVVNSLDGCKSCPSQEHMQSOPVQHLLIYKDCSDHYVLGRSSGAYRYTPDHRNS 229
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 67 dentvvdllgs-----krq-----yadceifndgyklsgfykikqlqspa 106
QY 230 -SFEVYCDMETMGCGTWTVLQARLDGSTNFTREWKDYKAGFNGLEREFWLGNDKIHLLT 286
| | | | | |||||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 107 efsvydcmsd-99gwtviqrrsdgsenfngwkdyengfngvqkhgcywlgknlnhflt 165
QY 287 KSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFSRH----- 341
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 166 tqedytlkldlafeknsryaqyknfkvgdekfnfyelnigeysgtagdsiagnfhpevqw 225
QY 342 -YNHDLRFPTTDRNDRYPSGNCGLIYSSGWFWFSCLSANLNGKYHOKYKGVN-VRNGIF 399
:| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 226 washqrmkfstwdrdhny-egnceaedgsgwwfnrchsanlngvyysgpytaktngiv 284
QY 400 WGTWPGINQAOQPGYKSSFKQAKMMIRPKNF 432
||| | |||||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
Db 285 wytw-----hgwwyslksvvmkirpndfip 309

RESULT 12
R94316
ID R94316 standard; Protein; 312 AA.
XX
AC R94316;
XX
DT 05-NOV-1996 (first entry)
XX
DE Hepatocyte proliferation substance HP-041.
XX
KW Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter;
KW chinese hamster ovary cell; CHO; hepatitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22 /note= "signal peptide"
FT Protein 23..312 /note= "mature protein"
XX
XX
PN WO9609383-A1.
XX
XX
PD 28-MAR-1996.
XX
XX
PF 21-SEP-1995; 95WO-JP01904.
XX
XX
PR 22-SEP-1994; 94JP-0228234.
XX
XX
PA (TAISHO ) TAISHO PHARM CO LTD.
XX
XX
PI Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;
XX
DR WPI; 1996-188445/19.
DR N-PSDB; T13396.
XX
XX
PT Vector for expression of hepatocyte proliferation substance - in
PT eukaryotic cells, used as diagnostic reagent for hepatitis and for
PT basic research on in vitro liver cell cultures
XX
PS Claim 2; Page 23-24; 44pp; Japanese.

```


XX PI Valenzuela DM;
 XX XX
 DR WPI; 1999-418933/35.
 DR N-PSDB; X85783.
 XX XX
 PT Receptor tyrosine kinase, AR-1 and related nucleic acid molecules
 XX XX
 PS Example 4; Fig 4A-B; 50pp; English.
 XX XX
 CC The present sequence represents a receptor tyrosine kinase, designated
 CC AR-1, which is related to TIE ligands. AR-1 is believed to be a
 CC regulator of angiogenesis and thus the factor, as well as nucleic acids
 CC encoding it, are useful in the diagnosis and treatment of certain
 CC diseases such as neoplastic diseases involving tumour angiogenesis,
 CC wound healing, thromboembolic diseases, atherosclerosis and inflammatory
 CC diseases. AR-1 can also be used to support the survival and/or growth
 CC and/or migration and/or differentiation of human AR-1 receptor expressing
 CC cells. AR-1 can be used to identify the AR-1 receptor. AR-1-cytotoxic
 CC conjugates can be used to target tumours expressing AR-1 or its receptor.
 CC Antagonists of AR-1, e.g. antibodies are useful to prevent or attenuate
 CC its biological activity.
 XX XX
 SQ Sequence 346 AA;

Query Match 21.7%; Score 507; DB 20; Length 346;
 Best Local Similarity 35.5%; Pred. No. 6.4e-37;
 Matches 123; Conservative 54; Mismatches 121; Indels 48; Gaps 14;
 QY 104 HRDPGGNGGNGAETADSRVOELSSQVKNLSSELK--NAKDOIQGLQGRLETLHL-VNMN 160
 Db 32 hktpaqqlkaancee--vkelkaqvanlssllselnkkqrdwsvvmqvmlesnsk 89
 QY 161 NIENYVDNKVANLTVVVNSLDGKCSKPSOEHMOSOPVOHL-----IYKDCSDHYVLG 213
 Db 90 rmesrltdaeskysemmnqid-----lmqlgaagtvtqttsadaily-dcsslyqkn 138
 QY 214 RRSGGAYRVTPDH--RNSSEFVYCDMETMGGWTVLQARLDGSTNFTREWKDYKAGFGL 271
 Db 139 yrisgvyklppddflgspellevfcdmetsgggwtliqrksglvsvfyrwkqykgfgsi 198
 QY 272 EREFWLGNDKIHLLTKSKEMILRIDLEPFGNLTLYALYDQFVYVANEFLKRLHIGNYGT 331
 Db 199 rgdflwlgnehlrlsrqptr-lrvemedwegnlryaeyshfvlgnelsyrlflgnytn 257
 QY 332 AG-DALFRSHYNHDLRFFTPDRDNDYPSGNCGLYSSGWWFDCSLSANLNGKY--- 387
 Db 258 vngdaly-----hntafstkdkndnc-ldkcaqlrkgygwyngcctdsnlngvyrlg 311
 QY 388 -HOKYKGVNRGIFWGTWPGINOAOPGGYKSSFKQAKMMIRPKNFKP 432
 Db 312 ehkh---ldgitwygwhgsty-----slkrvmekirpedfcp 346

RESULT 15

Y05399

ID Y05399 standard; Protein; 346 AA.

XX XX

AC Y05399;

XX XX

DT 01-JUL-1999 (first entry)

XX XX

DE Human TIE ligand NL4 protein sequence.

XX XX

KW Human TIE ligand; NL1; NL4; NL5; NL8; Ig homology domain; angiogenesis;
 KW EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
 KW early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
 KW endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;

KW vasculogenesis; detection; diagnosis; therapy.

XX XX

OS Homo sapiens.

XX XX

PN WO9915653-A2.

XX XX

PD 01-APR-1999.

XX XX

PF 14-SEP-1998; 98WO-US19093.

XX XX

PR 29-OCT-1997; 97US-0960507.

XX XX

PR 19-SEP-1997; 97US-0933821.

XX XX

PA (GETH) GENENTECH INC.

XX XX

XX Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;

PI Hillan K, Roy M, Schwall R, Tumas D;

XX XX

DR WPI; 1999-263480/22.

XX XX

DR N-PSDB; X36344.

XX XX

XX New isolated TIE ligand homologs for, e.g. developing products for

PT treatment of tumors

XX XX

PS Claim 8; Fig 14; 132pp; English.

XX XX

XX This sequence is the human tyrosine kinase containing Ig and EGF

CC homology domains (TIE) ligand of the invention, designated NL4.

CC The TIE receptors are receptor tyrosine kinases which are expressed in

CC vascular endothelial cells and early haemopoietic cells. The TIE

CC receptors are believed to be actively involved in angiogenesis, and may

CC play a role in haemopoiesis as well. The TIE ligand homologs can promote

CC the survival and/or growth and/or differentiation of TIE receptor

CC expressing cells. They can be used for promoting neovascularisation in

CC wound healing and for promoting angiogenic processes, such as for

CC inducing collateral vascularisation in an ischaemic heart or limb, or for

CC promoting bone development and/or maturation and/or growth in a patient

CC or muscle growth and development. The TIE ligand homologs and antibodies

CC can inhibit the growth of endothelial cells and induce apoptosis of

CC cells, particularly tumour cells. They can inhibit vasculogenesis,

CC particularly the vascularisation of tumour cells. The antibodies can also

CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,

CC NL8 or NL4 polypeptide is amplified. The products can also be used for

CC detection, diagnosis, drug screening and production of transgenic

XX XX

SQ Sequence 346 AA;

XX XX

XX Query Match 21.7%; Score 507; DB 20; Length 346;

XX Best Local Similarity 35.5%; Pred. No. 6.4e-37;

XX Matches 123; Conservative 54; Mismatches 121; Indels 48; Gaps 14;

QY 104 HRDPGGNGGNGAETADSRVOELSSQVKNLSSELK--NAKDOIQGLQGRLETLHL-VNMN 160

Db 32 hktpaqqlkaancee--vkelkaqvanlssllselnkkqrdwsvvmqvmlesnsk 89

QY 161 NIENYVDNKVANLTVVVNSLDGKCSKPSOEHMOSOPVOHL-----IYKDCSDHYVLG 213

Db 90 rmesrltdaeskysemmnqid-----lmqlgaagtvtqttsadaily-dcsslyqkn 138

QY 214 RRSGGAYRVTPDH--RNSSEFVYCDMETMGGWTVLQARLDGSTNFTREWKDYKAGFGL 271

Db 139 yrisgvyklppddflgspellevfcdmetsgggwtliqrksglvsvfyrwkqykgfgsi 198

QY 272 EREFWLGNDKIHLLTKSKEMILRIDLEPFGNLTLYALYDQFVYVANEFLKRLHIGNYGT 331

Db 199 rgdflwlgnehlrlsrqptr-lrvemedwegnlryaeyshfvlgnelsyrlflgnytn 257

QY 332 AG-DALFRSHYNHDLRFFTPDRDNDYPSGNCGLYSSGWWFDCSLSANLNGKY--- 387

Db 258 vngdaly-----hntafstkdkndnc-ldkcaqlrkgygwyngcctdsnlngvyrlg 311

QY 388 -HOKYKGVNRGIFWGTWPGINOAOPGGYKSSFKQAKMMIRPKNFKP 432

Db 312 ehkh---ldgitwygwhgsty-----slkrvmekirpedfcp 346

Search completed: February 27, 2001, 12:48:40
Job time: 65 sec

SPTREMBL 15:*

5: sp_invertebrate:*

Accession	Length (bp)	Species	Database
Q9p2y7	495	homo sapien	EMBL; 236531; CAA85298.1; -
Q9p2y7	22.8	homo sapien	DR

Q9u8w7	tachypleus
19	479
20.5	316
5	5
Q9u8w7	5

1 MRLPGWLSSAVLAACR-AVEEHNITEGLEDSAAQAACPARLEGGRC-EGSQCPFLT 58

Qy	181	DGRC	-----SKCPSEHQMQSPVQHLI	-----YKDCSDHYVLG	213
Db	231	EKKTVTAVNNSVLQKQKHDLMEVTNNLLTMNSTSNSKDP	PTVAKEEQISFRDCAEVFKSG	290	231
Qy	214	RRSSCAVYRTPDHRNSSFEVYCDMETGCGWTVLQARLDG	STNFTREMKDYKACFCGNLR	273	214
Db	291	HTTNGITVLTTPNSTEELKAYCDMEAGGWTII	ILORRDSGVDFQRTWKKEYKVGFGNPSG	350	291
Qy	274	EFWLGNDKIHLHTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYNTAG		333	274
Db	351	EYWLGNFVSVLTNQRYVLKILHKDWEGNEAYSLEYEHFVLSSEELNRYIHLKGLGTGAG		410	351
Qy	334	DALFRSHYHNDLRFFTPDPDNDNDRYPSGNCGLYYSGWTFDSCLSANLNGKYYHQYKKG		393	334
Db	411	KISSISOPGND-----FSTKGDGNDKIC-KCSQMLTGGMWFDACGPSNLNGMYYPQRNT		465	411
Qy	394	VR-NGIFWGTWPGINQAPGGYKSSFFQAKMMIRPKNF	430		394
Db	466	NKFGNGIKWYKKG-----SGY--SLKATTMMIRPADF	495		466
RESULT	5				
015123		PRELIMINARY;	PRT; 496 AA.		
AC	O15123				
ID	O15123				
DT	01-JAN-1998 (Tremblrel. 05, Created)				
DT	01-JAN-1998 (Tremblrel. 05, Last sequence update)				
DT	01-OCT-2000 (Tremblrel. 15, Last annotation update)				
DT	ANGIOPOIETIN-2.				
GN	ANGPT2.				
OS	Humo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Chordata; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC	NCBI TaxID=9606.				

NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RC
PC TISSUE=LUNG;
RX MEDLINE=97349327; PubMed=9204895;
RA Maisonneire P.C., Suri C., Jones P.F., Bartunkova S., Wlegand S.J.,
RA Radzietjewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RL Science 277:55-60(1997).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS
CC FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC
CC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX
CC CONTRACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT
CC VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE
CC ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A
CC PERMISSIVE ANGIOGENIC SIGNAL.
CC -1- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.

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DR MM; 601922; -.
DR INTERPRO; IP0002181; -.
DR PFAM; PF001147; fibrinogen.C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Coiled coil.
FT DOMAIN 55 58 POLY-SER.
FT DOMAIN 130 256 COILED COIL (POTENTIAL).
FT DOMAIN 282 496 FIBRINOGEN BETA/GAMMA.
FT DOMAIN 318 321 POLY-GLY.
SQ SEQUENCE 496 AA; 56919 MW; 5642A58847A7385C CRC64;

Query Match 22.8%; Score 533.5; DB 4; Length 496;
Best Local Similarity 29.4%; Pred. No. 6.9e-32;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps

QV 48 CEGSQCPF-----QLTPTLTITLQIPLQSGMEEVLKE----VRLTKEAV-DSLKKSCDQC 97

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Db 53 CRSSSPVSVNAVQDAPLEYDDSVQRLOVLENNINNTQWLKLENTIODNNKKEWVEI 112
QY 98 KLQADHR-----DPGGNGGNGAETASDR-VOELESQV-----NKL 133
Db 113 QONAVQNTAVMIETGTLLN--QTAEQTKLTDEVAQVLTOTRLEQLLHLSLSTNKL 170
QY 134 SSELKNADJOILOGGR-----LETLHLVNMNIENYVDN--KVALNTVVVNSL 180
Db 171 EKQILDQTSINKLDKNSFLEKKVLAEMDKHIIQLOSIKEEKDQQLVLSKNSIIEL 230
QY 181 DGKC-----SKPQSBHMSQPVQHLI-----YKDCSDHYVL 212
Db 231 EKKIVTATVNSVLQKQHDLMETVNNLLTMMSTNSAKDPTVAKEEQISFRDCAEVFS 290
QY 213 GRRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQARLDGSTNFTREWKDYKAGFNS 272
Db 291 GHTTNGIYTLTFPNSSTEEIKAYCDMEAGGGWTIIORREDGSDVDFQRTWKYKVGFGNS 350
QY 273 REFVLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYTA 332
Db 351 GEYWLGNFEVFSQLTNQRYVVKIHLKDWEGNEAYSLEYHFLSSSEELNYRIHLKGLTGA 410
QY 333 GDALRFESHYNDLRFETTPDRNDYPSGNCGLYSSGWFDSCLSANLNGKYKHOKYK 392
Db 411 GKISSISQPGND----FSTKGDNDKIC-KCSQMLTGGWFDACGSPNLNGMYTPORON 465
QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKQAKMIRPKNF 430
Db 466 TNKFNKGIKWTYWKG-----SGY--SLKATMMIRPADF 496
RESULT 6
Q9PU54
ID Q9PU54 PRELIMINARY; PRT; 407 AA.
AC Q9PU54;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANGIOPOIETIN-2 (ANG-2B).
GN ANGIOPOIETIN-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HUBBARD WHITE MOUNTAIN;
RA Mezquita J., Mezquita B., Pau M., Mezquita C.;
RT "Characterization of a novel form of angiotensin-2 (Ang-2B) and
RT expression of VEGF and angiotensin-2 during chicken testicular
RT development and regression."
RL Biochem. Biophys. Res. Commun. 260:492-498(1999).
DR EMBL: AJ31923; CAB59200.1; -.
DR HSSP: P02671; IFFZD.
DR INTERPRO: IPR002181; -.
DR PFAM: PF00147; fibrinogen.C; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN: 1.
SQ SEQUENCE 407 AA; 46647 MW; E10C03D07E410013 CRC64;
Query Match 22.7%; Score 532; DB 13; Length 407;
Best Local Similarity 33.8%; Pred. No. 6,9e-32;
Matches 136; Conservative 62; Mismatches 130; Indels 74; Gaps 14;
QY 63 TIQIPRQLSME-EVLKEVRTLKEAVDSLKSCDCKLQADHRDPGGNGGNGAETASDR 121
Db 46 TAEQTKLTDEVAQVLTOTRLE--LQLEHLSLSTNKLREQ-----ISVQTEIT 93
QY 122 RVOE-----LESQVKNLSSE-----LKNADQIOGLOGLRLETLHLVNMNIENYVDN 170
Db 94 KLQEKNSFLEKRVLEMDKHTLQLKSIDKEDQQLVLA-----QNSIIELEKOL 145

QY 171 ANLTVVNSLDGKCKSCPSQEHMQSPVQHLI-----YKDCSDH 209
Db 146 --VATVNN-----SVLQKQHDLMETVNNLLTMMSTNSAKNFIAKEQISFKDCAEA 198
QY 210 YVLGRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQARLDGSTNFTREWKDYKAGFG 269
Db 199 FKSGLTSGTYTLTFPNSAQEKAYCDMESNGGWTVLRREGGSVDFFHRTWKYKIGFG 258
QY 270 NLREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYN 329
Db 259 DPAGEWLGNEFVSQLTNQRYVVKIHLKDWEGNEAYTLTYDQFYLANEEOKYRIHLKGLT 318
QY 330 GTAGDALRFSRHYNDLRFETTPDRNDYPSGNCGLYSSGWFDSCLSANLNGKYHYQ 389
Db 319 GTAGKISSISQPGND----FSTKGDNDKIC-KCSQMLTGGWFDACGSPNLNGMYTPI 373
QY 390 KYGVR-NGIFWGTWPGINQAPGGYKSSFKQAKMIRPKNF 430
Db 374 RONNKFNGIKWTYWKG-----SGY--SLKATMMIRPADF 407
RESULT 7
Q9NR7
ID Q9NR7 PRELIMINARY; PRT; 444 AA.
AC Q9NR7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANGIOPOIETIN-2 ISOFORM-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Mah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiotensin-2."
RL J. Biol. Chem. 275:18550-18556(2000).
DR EMBL: AF187858; AAF76526.1; -.
SQ SEQUENCE 444 AA; 50958 MW; E512409CE73987A1 CRC64;
Query Match 22.4%; Score 524.5; DB 4; Length 444;
Best Local Similarity 34.6%; Pred. No. 2.8e-31;
Matches 118; Conservative 57; Mismatches 119; Indels 47; Gaps 9;
QY 116 ETAEDSRVOELESQVKN--LSSE-----LKNADQIOGLOGLRLETLHLVNMNIEN 164
Db 125 QTSEINKLQDKNSFLEKKVLAEMDKHIIQLOSIKEEKDQQLVLSK-----QNSIIE 176
QY 165 YVDNKVANLTV-----VVNSLDGKCKSCPSQEHMQSPVQHLIYKDCSDHY 210
Db 177 ELEKKIVTATVNNSVLQKQHDLMETVNNLLTMMSTNSAKDPTVAKEEQISFRDCAEV 236
QY 211 VLGRSSGAYRVTDPHRNSSFEVYCDMETGGWTVLQARLDGSTNFTREWKDYKAGFGN 270
Db 237 KSCHTNGIYTLTFPNSSTEEIKAYCDMEAGGGWTIIORREDGSDVDFQRTWKYKVGFGN 296
QY 271 LEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTYALYDQFYVANEFLKYRLHIGNYN 330
Db 297 PSCEYWLGNFEVFSQLTNQRYVVKIHLKDWEGNEAYSLEYHFLSSSEELNYRIHLKGLT 356
QY 331 TAGDALRFSRHYNDLRFETTPDRNDYPSGNCGLYSSGWFDSCLSANLNGKYHYQ 390
Db 357 TAGKISSISQPGND----FSTKGDNDKIC-KCSQMLTGGWFDACGSPNLNGMYTPOR 411
QY 391 KYGVR-NGIFWGTWPGINQAPGGYKSSFKQAKMIRPKNF 430
Db 412 QNTNKFNGIKWTYWKG-----SGY--SLKATMMIRPADF 444

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RESULT 8
Q08830 PRELIMINARY; PRT; 312 AA.
AC Q08830;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR.
GN HFRP-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=HEPATOMA;
RX MEDLINE=93290661; PubMed=8390249;
RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA Hirohashi S.;
RT "Molecular cloning and initial characterization of a novel fibrinogen-
RT related gene, HFRP-1."
RL Biochem. Biophys. Res. Commun. 193:681-687(1993).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
CC -!- TISSUE SPECIFICITY: OVEREXPRESSED IN HEPATOCELLULAR CARCINOMAS.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL: D14446; BAA03336.1; -
DR HSSP: P02671; LFZD.
DR INTERPRO: IPR002181; -
DR PFAM: PF00147; fibrinogen_C; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Plasma; Blood coagulation; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 312 FIBRINOGEN-LIKE PROTEIN 1.
FT SIMILAR 70 296 BETA/GAMMA CHAINS OF FIBRINOGEN.
FT DISULFID 83 112 BY SIMILARITY.
FT DISULFID 248 261 BY SIMILARITY.
SQ SEQUENCE 312 AA; 36378 MW; 2330F3D6C0D0BBA8 CRC64;

Query Match 22.2%; Score 519.5; DB 4; Length 312;
Best Local Similarity 33.8%; Pred. No. 4.2e-31;
Matches 131; Conservative 47; Mismatches 117; Indels 93; Gaps 11;

QY 55 FQLTLPTLTQLPQLGSMEEVLKEVTLKFAVDSLKSKSCODCKLQADDDHDPGNGGNG 114
DB 5 FSPILVTALIMGREISALEDCAQEQMRLRAQVRL----- 40

QY 115 AETAEDSRVQELSSQVKNLSSELKNAKDQIQGLQGRLETLHLVNMNIENYVDNKVANLT 174
DB 41 -----ETRVKQQVKIKQLQE-----NEVQFL-----DKGDEDT 70

QY 175 VVNSLDGKCKPCSPQEHMQSPVQHLYIKDCSDHYVLGRRSSGAYRVTPDHRNSSFEVY 234
DB 71 VV--DLGSRQ-----YADCSIFNDGYKLSGYKIKPLQSPAESVY 111

QY 235 CDMEYGGGTVLQARLDGNTFTREWKDYKAGFNLER---EFWLGNDKIHLLTKSKEM 291
DB 112 CMDS--GGGTVTQRRSDGSFENFRGKDYENGFGNFVQRHGEYWLGNKLNHLFTTQEDY 170

QY 292 ILRIDLEDFNGLTYALYDQFYVANEFLKYLHGTNGYTAGDALRFSRH-----YNHD 345
DB 171 TLKIDLADEFKNRYAQYKNFKVDEKFNFYELNIGESYSGTAGDSLGNFHPFVQWASHQ 230

QY 346 LRFFTTPDRDNDRYPSGNCGLLYTSSGWFSDCLSANLNGKYHOKYKYG--VRNGIFWGTWP 404
DB 231 RMKFSTWDRHDNY--EGNCAEEDQSGWFRNCHSANLNGVYISPYTAKTDGLVWTW-- 288

QY 405 GINQAPGGYKSSFKQAKMMIRPNKFP 432
DB 289 -----HGWWYSLKSVVMKIRPNDFIP 309
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RESULT 9
Q09UW8 PRELIMINARY; PRT; 292 AA.
AC Q09UW8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE TECHLECTIN-5A.
OS Tachyplesus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachyplesus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
RA Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.;
RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
RT immunity are structurally related to fibrinogen."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
DR EMBL: AB024737; BAA84188.1; -
DR HSSP: P02671; LFZD.
DR INTERPRO: IPR002181; -
DR PFAM: PF00147; fibrinogen_C; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 292 AA; 33786 MW; D028DE1E2716F71A CRC64;

Query Match 21.9%; Score 513.5; DB 5; Length 292;
Best Local Similarity 42.7%; Pred. No. 1.1e-30;
Matches 103; Conservative 38; Mismatches 81; Indels 19; Gaps 6;

QY 195 SQPVQHLVYKDCSDHYVLGRRSSGAYRVTPDH--RNSSEVYCDMETGSGWTVLQAR-- 250
DB 61 ADPIVSPDPTDCADLLNGYRSGGRIWPKSWMTVGLNLYCDMETDGGWTVIQRGN 120

QY 251 -LDGSTNFTREWKDYKAGFNLEREFWLGNDKIHLLTKSKEMILRIDLEDFNGLTYALY 309
DB 121 YGNPSDYFYKPKWKYKLGFGNIEKDFWLGNDRIALTQNRNYMIRFDLKDENDTRYAIY 180

QY 310 DQFYVANEFLKYLHGTNGYTAGDALRFSRHYNHDLRFTTPDRDNDRYPSGNCGLLYS 369
DB 181 QDFWIENEDYLYCLHGTNGYSGDAGNS--FGRHNGHN---FSTIDKDHDTHT--HCAQTYK 234

QY 370 SGWFFSDCLSANLNGKYHOKYKYGVRNGIFWGTWPCINQAOQPGYKSSFKQAKMMIRPN 429
DB 235 GGMWYDRCHESNLNGLYNGEHSYADGIEWRAWK-----GYHSLPQVEMKIRPVE 286

QY 430 F 430
DB 287 F 287

RESULT 10
Q043827 PRELIMINARY; PRT; 346 AA.
AC Q043827;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CDP6.
GN DJ647M16.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=CORNEA;
RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baggualee C.;
```


RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RT	Sato S., Nagase T., Seki N., Ishikawa K.I., Tabata S.;
RT	"Prediction of the coding sequences of unidentified human genes. I.
RT	The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT	analysis of randomly sampled cDNA clones from human immature myeloid
RT	cell line Kg-1 (supplement).";
RL	DNA Res. 1:47-56(1994).
CC	-I- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING TIE2
CC	TYROSIENE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC	PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC	CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC	ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC	VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC	HEART EARLY DEVELOPMENT.
CC	-I- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC	IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
CC	PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC	ISCHEMIC HEART.
CC	-I- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC	THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
CC	-I- PTM: GLYCOSYLATED.
DR	EMBL; U83508; AAB50557.1; -
DR	ENBL; D13628; BAA02793.1; -
DR	HSSP; P02671; IFZD.
DR	MIM; 601667; -
DR	INTERPRO; IPR002181; -
DR	PFAM; PF00147; fibrinogen_C.1.
DR	-PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW	Glycoprotein; Coiled coil.
FT	DOMAIN 81 119 COILED COIL (POTENTIAL).
FT	DOMAIN 153 261 COILED COIL (POTENTIAL).
FT	DOMAIN 284 498 FIBRINOGEN BETA/GAMMA.
FT	CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE 498 AA: 57513 MW; 5D5FA63AEF6BE920 CRC64;
Query Match 20.9%; Score 489; DB 4; Length 498;	
Best Local Similarity 31.1%; Pred. No. 1.4e-28;	
Matches 137; Conservative 70; Mismatches 145; Indels 88; Gaps	
QY	19 AVEHNLT-----TEGLEDSAAQAACPARGSGRCESGPCFLTPTLT-TIOLPQ-L 70
DB	: :
DB	119 AVONHTATMETGTSLLSQTAEOTRKLTDFEVQLVNTSRLEIGLLENSLTYLEKQLL 178
DB	:
QY	71 GSMEEVLK--EVRTL-----KEAVDSLKKSCQDCKLQADHRDPGGNGGAE 116
DB	
DB	179 QQTNEILKTHKSNLLEKHILEMEGKHKEELDTLKEKENLNQ-----GLV 223
DB	
QY	117 TAEDRSVOELSEOVNKLSELKNAKDOIGLOGRLETLH-LVNMMNIENYDNKANVTV 175
DB	: : : : : :
DB	224 TRQTYTIOELEKOLNRATT--NNSVLKQOOLE-LMDTVHNLNL----- 264
QY	176 VNNSLDGCKSK---CPSEEHMOSOPVQHLIYKDCSDHVVLGRRSSGAYRVTPDHNSSF 231
DB	
DB	265 -----CTKEGVLLKGREEPK-----FRCDADVTAQFNKSGIYTIYNMPEPK 311
QY	232 EYVCDMETMGGWTVLQARDLGSTNFTREWQDKAGFNLEREFWLGNKDHIHLTKSKEM 291
DB	: : :
DB	312 KVCNCNDVNGGGWTVLQHREDGSLDLFQRCWKKEYKMFGPNPSGEYLWGNFEIFATSQRQY 371
QY	292 ILRIDLEDNFGLTLYALXDQFYVANETFKYRIUHGNYNGTAGDALRFSRHYNHDLRFFTT 351
DB	: : : : : : : : : : :
DB	372 MLRIELMDWEGNRAYSQYDRFHIGNEKONYRLYLXGHGTAGKQSSLILH-GAD---FST 427
QY	352 PDQNDRIYPSGNCGLYSYGWWFDSCLSANLNGKYHQ-KYGYVRNGIFPWGTWPGINQAO 410
DB	
DB	428 KDADNDNCMC-KCALMLTCGGWFDA CGPSNLNGMYFTAQNHGKLNGIKWHYFKGPSY-- 484
QY	411 PGGYKSSFKQAKMWIRPKNF 430

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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:48:04 ; Search time 21.07 Seconds
(without alignments)
368.175 Million cell updates/sec

Title: US-09-442-143-4
Perfect score: 2340
Sequence: 1 MRLPCWLWSSAVLAACRAV.....GYKSSFQKAKMIRPKFKP 432

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	533.5	22.8	314	1	US-08-525-505A-2	Sequence 2, Appli
2	533.5	22.8	496	1	US-08-373-579-6	Sequence 6, Appli
3	533.5	22.8	496	2	US-08-418-595-6	Sequence 6, Appli
4	533.5	22.8	496	2	US-08-665-926-6	Sequence 6, Appli
5	533.5	22.8	496	3	US-09-162-437-6	Sequence 6, Appli
6	524	22.4	312	1	US-08-525-505A-4	Sequence 4, Appli
7	509	21.8	286	3	US-08-960-507-20	Sequence 20, Appli
8	507	21.7	346	3	US-08-960-507-19	Sequence 19, Appli
9	489.5	20.9	497	1	US-08-373-579-4	Sequence 4, Appli
10	489.5	20.9	497	2	US-08-418-595-4	Sequence 4, Appli
11	489.5	20.9	497	2	US-08-665-926-4	Sequence 4, Appli
12	489.5	20.9	497	2	US-08-348-492-4	Sequence 4, Appli
13	489.5	20.9	497	3	US-09-162-437-4	Sequence 4, Appli
14	488.5	20.9	453	1	US-08-206-176-6	Sequence 6, Appli
15	488	20.9	491	3	US-08-933-821-4	Sequence 4, Appli
16	488	20.9	491	3	US-08-960-507-4	Sequence 4, Appli
17	483.5	20.7	493	2	US-08-933-821-2	Sequence 2, Appli
18	483.5	20.7	493	3	US-08-960-507-2	Sequence 2, Appli
19	483	20.6	498	1	US-08-373-579-2	Sequence 2, Appli
20	483	20.6	498	2	US-08-418-595-2	Sequence 2, Appli
21	483	20.6	498	2	US-08-665-926-2	Sequence 2, Appli
22	483	20.6	498	2	US-08-348-492-2	Sequence 2, Appli
23	483	20.6	498	3	US-09-162-437-2	Sequence 2, Appli
24	480.5	20.5	411	1	US-08-232-532-1	Sequence 1, Appli
25	480.5	20.5	411	2	US-08-748-150-1	Sequence 1, Appli
26	480.5	20.5	411	4	PCT-US95-05168-1	Sequence 1, Appli
27	471.5	20.1	509	2	US-08-665-926-8	Sequence 8, Appli
28	465.5	19.9	454	3	US-08-434-099A-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1
US-08-525-505A-2
; Sequence 2, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAEO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPATOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCQUELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-525-505A-2

Sequence 28, Appli
Sequence 49, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 21, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 5, Appli

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-373-579-6

Query Match          22.8%; Score 533.5; DB 1; Length 496;
Best Local Similarity 29.4%; Pred. No. 3.7e-43;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps

QY 48 CEGSQCPF-----QLTLPITLTIQLPRLGSMEEVLKE---VRTLKEAV--DSLKSKQCQC 97
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Db 53 CRSSSPYVSNVAVORDAPLEYDDSVQRLQVLENNMTQWLAKLENYIQDNKKKEWEI 112
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QY 98 KLQADHR-----DPGNGGNGAETADSR-VOELSESQV-----NKL 133
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Db 113 QONAVQNOTAVMIEIGTNLLN--QTAEQTRKLTDEVAQVNLQNTTRLELQILLEHSLSTNKL 170
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QY 134 SSELKNAKDQIQLOGR-----LETLHLVNMNNIENYVDN--KVANLTVVVVNSL 180
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Db 171 EKQILDQTSINKLQDKNSFLEKKVVLAMEDKHIIQSQSKEEKDQQLVLVSKNSIIIEEL 230
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QY 181 DGRC-----SKPCSPHEHMQSPQVHIL-----YKDCSDHYVL 212
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Db 231 EKKIVTAVNSVLQKQOHDLMETVNNLLTMMSTNSAKDPTVAKBEQISFRCAEVFKS 290
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QY 213 GRSSGAYRVTPHRRNSSFEVYCDMETMGWGWTVLQARLDGSTNFTREWKDYKAGFNL 272
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Db 291 GHTTNGITTYITLTFPNSTEIKAYCDMEAGGGGWTIIQRREDGSDVFQRTWKKEYKVGFGNPS 350
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Db 411 GKTSISQPGND---FSTKDGNDKIC--KCSQMLTGGWWFADACGPNLNGMYYPQRQN 455
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QY 393 GVR-NGIFGWTWPGINQAOPGGYKSSFKQAKMIRPKNF 430
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RESULT 3
US-08-418-595-6
; Sequence 6, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595
; FILING DATE: 06-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579

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FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-418-595-6

Query Match 22.8%; Score 533.5; DB 2; Length 496;
Best Local Similarity 29.4%; Pred. No. 3.7e-43;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CEGSQCPE-----QLTPTLTITQLPRLGSMEEVLKE---VRTLKEAV-DSLKSKCQDC 97
DB 53 CRSSSPYVNAVQDAPLEYDDSVORLOVLENNMTQWLKLENYIQDNMKKEMVEI 112
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DB 113 QONAVONQAVMIEIGTNLLN--QTAEQTRKLTDEVAQVLNQTTRLEQLLHLSLSTNKL 170
QY 134 SSELKNADQIOGLOGR-----LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
DB 171 EKQILDQTSSEINKLQDNKSFLEKRVLAMEDKHIIQLOSIKEEKDQLQVLVSKNSIIEEL 230
QY 181 DGKC-----SKCPSOEHMOSQPVQHLI-----YKDCSDHYVL 212
DB 231 EKKIVTATVNNSVLQKQOQDLMTETVNNLLTMSTNSAKDPTVAKEEQISFRDCAEVFKS 290
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DB 291 GHTNGIYTLTPNSTEIKAYCDMEAGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPS 350
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QY 333 GDALRFSRHYNDLRFPTTDRNDNDRYPGNCGLIYSSGWWFDCSLSANLNGKYYHOKYK 392
DB 411 GKISSISQPGND-----FSTKGDNDKIC-KCSQMLTGGWWFDCAGPSNLNGMYYPQRN 465
QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKQAKMMIRPKNF 430
DB 466 TNKFNKIKWYKKG-----SGY--SLKATMMIRPADF 496

RESULT 4
US-08-665-926-6
Sequence 6, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-6

Query Match 22.8%; Score 533.5; DB 2; Length 496;
Best Local Similarity 29.4%; Pred. No. 3.7e-43;
Matches 135; Conservative 80; Mismatches 153; Indels 91; Gaps 16;

QY 48 CEGSQCPE-----QLTPTLTITQLPRLGSMEEVLKE---VRTLKEAV-DSLKSKCQDC 97
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QY 98 KQADDDR-----DPGGNGGNGAETAEDSR-VOELESQV-----NKL 133
DB 113 QONAVONQAVMIEIGTNLLN--QTAEQTRKLTDEVAQVLNQTTRLEQLLHLSLSTNKL 170
QY 134 SSELKNADQIOGLOGR-----LETLHLVNMNNIENYVDN---KVANLTVVVNSL 180
DB 171 EKQILDQTSSEINKLQDNKSFLEKRVLAMEDKHIIQLOSIKEEKDQLQVLVSKNSIIEEL 230
QY 181 DGKC-----SKCPSOEHMOSQPVQHLI-----YKDCSDHYVL 212
DB 231 EKKIVTATVNNSVLQKQOQDLMTETVNNLLTMSTNSAKDPTVAKEEQISFRDCAEVFKS 290
QY 213 GRSSGAYRVTPDHRNSSFEVYCDMETMGGGWTVLQARLDGSTNFTREWKDYKAGFGNLE 272
DB 291 GHTNGIYTLTPNSTEIKAYCDMEAGGGWTIIQRREDGSDVDFQRTWKYKVGFGNPS 350
QY 273 REFVLGNDKIHLLPKSKEMILRIDLEDFNGLTYALYDQFYVANEFKLYRLHIGNYNGTA 332
DB 351 GEYWLGNFVSQLTNQORYVLKIHLDKWEAGNEAYSLYEHFVLSSEELNYRIHLKGLTGT 410
QY 333 GDALRFSRHYNDLRFPTTDRNDNDRYPGNCGLIYSSGWWFDCSLSANLNGKYYHOKYK 392
DB 411 GKISSISQPGND-----FSTKGDNDKIC-KCSQMLTGGWWFDCAGPSNLNGMYYPQRN 465
QY 393 GVR-NGIFWGTWPGINQAPGGYKSSFKQAKMMIRPKNF 430
DB 466 TNKFNKIKWYKKG-----SGY--SLKATMMIRPADF 496

RESULT 5
US-09-162-437-6
Sequence 6, Application US/09162437

Patent No. 6166185
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PS-09-162-437-6

[illegible]

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QY 213  GRESSGAYRVPDHRNSSFEVYCDMETGCGWTVLQARLDGSGTNETREWKDYKAGFGNLE 272
Db 291  GHTNYGLYUFTFNSTEEIKAYCDMEAGGGWTFIQRRDGSVDFTWKETKVGFGNPS 350
QY 273  REFWLGNDKIHLTKSKEMILRIDLEDFNGLTLYALYDOFYVANEFKYRLHIGNYNGTA 332
Db 351  GEYWLGNFEVSQLTNOORYVLKHLKDWEGNEAYSLEYHFYLSSELNRYRIHLKGLTGTA 410
QY 333  GDALRSRHYNDLREFTTTPDRDNDRIYPSGNCGLYYSSGWNFSDCLSNLNGKYYHQYK 392
Db 411  GKTISSIQPGND---FSTKDGDNKCI-C-KCSQMLTGGWFDACGPSNLNGMYTPQRQN 465
QY 393  GVR-NGFWCTWPGINOAOPGGYKSFSSKQAKMMIRKPNF 430
Db 466  TNFNGIKWYWKG-----SGY--SLKATMMIRPADF 496

RESULT 6
US-08-525-505A-4
; Sequence 4, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAEKO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-525-505A-4

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Query Match 22.4%; Score 524; DB 1; Length 312;
Best Local Similarity 37.8%; Pred. No. 1.5e-42;
Matches 126; Conservative 41; Mismatches 114; Indels

2

[illegible]

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RESULT 7
US-08-960-507-20
Sequence 20, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy d
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960.507
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: pl130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
US-08-960-507-20

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Qy	187	CPSDEHMQSOPVQHLYIKDCSDHYVLGRRSSGAYRVTDPDRNSSFEYCDMETMGGGWTV	249
Db	55	SNSAKDPTVAKEEQISFRDCAEVFKSGHTTNGIYTLTFPNSTEEIKAYCDMEAGGGWTI	114
Qy	247	LQALDGSFTNTRWKDYKAGFGNLEREFWLGNDKHLHLTKSKEMILRLDLEDNFGLTLY	306
Db	115	IQRDEGSVDFOFTWKKEYKVGFGNPSEGYWLGNIEFVSQLTNOORYVLKHLKDWEGNEAY	174
Qy	307	ALYDOEYVANEFLKLHIHIGNYCTAGDALRFSRSHYNHDLRFTTPDRDNDRYPSCNCGL	366
Db	175	SLYEHFVLSSEELNYRIHLKGLGTAGKISSIQPGND-----ESTKDGDNDCIC-KCSQ	229
Qy	367	YYSGGWFDSCLSANLNGKYHKYKGVR-NGIFWGTPGINOAPGGYKSSFKAOKMMI	425
Db	230	MLTGWWFDCGSPNLNGMYPPQORNTKNENGLKWYWKG-----SGY--SLKATMMI	281
Qy	426	RPKNF 430	
Db	282	RPADF 286	
RESULT 8			
US-08-960-507-19			
; Sequence 19, Application US/08960507			
; Patent No. 6057435			
; GENERAL INFORMATION:			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; TITLE OF INVENTION: Tie Ligands			
; NUMBER OF SEQUENCES: 24			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Genentech, Inc.			
; STREET: 1 DNA Way			
; CITY: South San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94080			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: WinPatIn (Genentech)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/960,507			
; FILING DATE:			
; CLASSIFICATION: 536			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Dreger, Ginger R.			
; REGISTRATION NUMBER: 33,055			
; REFERENCE/DOCKET NUMBER: P1130pl			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 650/225-3216			
; TELEFAX: 650/952-9881			
; INFORMATION FOR SEQ ID NO: 19:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 346 amino acids			
; TYPE: Amino Acid			
; TOPOLOGY: Linear			
US-08-960-507-19			

```
Query Match      21.8%; Score 509; DB 3; Length 286;
Best Local Similarity 36.1%; Pred. No. 3.6e-41;
Matches 110; Conservative 48; Mismatches 111; Indels 36; Gaps 7;

OY 141 KDQFGQLGRLETHLVNMRNIENVONKANTV-----VVNSLDGRCCK 186
||| || | : | : | : | : | : | : | : | : | : | : | : | : |
db 3 KDQLQVLVSK-----QNSIIEELKKITATVNNSVLQKQOHLMETVNNLTWMTST 54
```


OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-418-595-4

Query Match 20.9%; Score 489.5; DB 2; Length 497;
Best Local Similarity 31.2%; Pred. No. 6.6e-39;
Matches 137; Conservative 70; Mismatches 145; Indels 87; Gaps 17;

QY 19 AVEEHLN-----TEGEDASQAACPARLEGSGRCGSCPPFOLTPTL-TIOLPRO-L 70
DB 119 AVONHTATMLEIGTSLSQTAEOTRKLTDTVETQVNLNSTRLEIQLENSLSTYKLEKQLL 178
QY 71 GSEEEVLK--EVRTL-----KEAVDSLKSKCQDCKLQADDDHDPGGNGGAE 116
DB 179 QQTNEILKHEKNSLLEHKEGKHKEELDTLKEKENLQ-----GLV 223
QY 117 TAEDSRVQELSQVKNLSSELKNAKDQIQGLGRLETLH-LVNMNNIENYVDNKVANLTV 175
DB 224 TROTYYIQELEKQLNRATT--NNSVLQKQOLE-LMDTVHNLVNL----- 264
QY 176 VVNSLDGKCSK---CPSQEHMQSQPVQHLIYKDCSDHYVLGRSSGAYRTPDHRNSSFE 232
DB 265 -----CTKEVLLKGGKREEDKP-----FRCDADYVQAGFNKSGIYTIYINNPEPKK 311
QY 233 VYCDMETMGGWTVLQARLDGSTNFTREWKDYKAGFNLEREFWLGNDKHLTKSKEMI 292
DB 312 VFCNMVNGGWTVIQHREDGSLDFQGWKEYKMGFNPGEYWLGNFEFAITSQRYM 371
QY 293 LRIDLEDFNLTYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFRSHYHDLRFFFTTP 352
DB 372 LRLELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGGTGTAGKQSSLLH-GAD---FSTK 427
QY 353 DRDNDYPSGNCGLYYSSGWFWFDSCLSANLNGKYHQ-KYKGVNRGIFGWTWPGINQAOP 411
DB 428 DADNDNMC-KCALMTGGWFWFACGPNLNGMFYTAGQNHGKLGKIKWHYFKGPSY--- 483
QY 412 GGYKSSFKQAKMIRPKNF 430
DB 484 -----SLRSTTMMIRPLDF 497

RESULT 11
US-08-665-926-4
Sequence 4, Application US/08665926
Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-4

Query Match 20.9%; Score 489.5; DB 2; Length 497;
Best Local Similarity 31.2%; Pred. No. 6.6e-39;
Matches 137; Conservative 70; Mismatches 145; Indels 87; Gaps 17;

QY 19 AVEEHLN-----TEGEDASQAACPARLEGSGRCGSCPPFOLTPTL-TIOLPRO-L 70
DB 119 AVONHTATMLEIGTSLSQTAEOTRKLTDTVETQVNLNSTRLEIQLENSLSTYKLEKQLL 178
QY 71 GSEEEVLK--EVRTL-----KEAVDSLKSKCQDCKLQADDDHDPGGNGGAE 116
DB 179 QQTNEILKHEKNSLLEHKEGKHKEELDTLKEKENLQ-----GLV 223
QY 117 TAEDSRVQELSQVKNLSSELKNAKDQIQGLGRLETLH-LVNMNNIENYVDNKVANLTV 175
DB 224 TROTYYIQELEKQLNRATT--NNSVLQKQOLE-LMDTVHNLVNL----- 264
QY 176 VVNSLDGKCSK---CPSQEHMQSQPVQHLIYKDCSDHYVLGRSSGAYRTPDHRNSSFE 232
DB 265 -----CTKEVLLKGGKREEDKP-----FRCDADYVQAGFNKSGIYTIYINNPEPKK 311
QY 233 VYCDMETMGGWTVLQARLDGSTNFTREWKDYKAGFNLEREFWLGNDKHLTKSKEMI 292
DB 312 VFCNMVNGGWTVIQHREDGSLDFQGWKEYKMGFNPGEYWLGNFEFAITSQRYM 371
QY 293 LRIDLEDFNLTYALYDQFYVANEFLKYRLHIGNYNGTAGDALRFRSHYHDLRFFFTTP 352
DB 372 LRLELMDWEGNRAYSQYDRFHIGNEKQNYRLYLKGGTGTAGKQSSLLH-GAD---FSTK 427
QY 353 DRDNDYPSGNCGLYYSSGWFWFDSCLSANLNGKYHQ-KYKGVNRGIFGWTWPGINQAOP 411
DB 428 DADNDNMC-KCALMTGGWFWFACGPNLNGMFYTAGQNHGKLGKIKWHYFKGPSY--- 483
QY 412 GGYKSSFKQAKMIRPKNF 430
DB 484 -----SLRSTTMMIRPLDF 497

RESULT 12
US-08-348-492-4
Sequence 4, Application US/08348492
Patent No. 5879672
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York

Db		101	KP-----NMIDAAATLKSR I--MLEEIMKMYEASILTHDSSSTRYLQ-----EYNSNN-----144
Qy		165	YVDNKVANLTWVWNLSLCKGCKSKCPSEQHMSQPVOHLIYKDCSDHVLVLRSSSGAYRVTP 224
Db		145	--QKIYNLKEKVAQLAEAOCE-QPKDTVQ---IHDLTGKCDODIANKAQOSGLYFIKP 197
Qy		225	DHRNSSFEVYCDMETGGGWTVLQARLDGSTNTRWKDYKAGFNLE----REFWLGN D 280
Db		198	LKANQQFLVTCEIDGSNGWTVFQKRUDGSVDFRKNWIYKEGFHLSPGTTFEFWLGNE 257
Qy		281	KIHLLTKSEM--TLRLDLEDNFLTLALYDGYVANEELFKYLRHLIGNY-NGTAGDAL- 336
Db		258	KIHLLISTQSAIPYALRYVELEDWNGRTSTADYAMFKVGP EADKYRLTVAYFAGGDGADEF 317
Qy		337	-----RFSRHYNHDLRFETTPDRDNDRYPSCNGCLYYSGGWHVFDSL SANLINGKY 386
Db		318	GFDGEDDPDSKF--FTSHNGMQTSTWDNDKPF-EGNCBAEQDGSGWMNKHCHAGHLGVY 374
Qy		387	YH-----QIKYKVRNRGI EWGTPGINOAQPGGYKS--SFRQAOKHMIRPKN 429
Db		375	YOGGTYSKASTPNCYDNGIIITWAYT-----KTRYWSMKTMTWKIIFEN 416

```

RESULT 15
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb fl
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933-821

```

```

>>> APPLICATION NUMBER:  US/08/933,821
>>> FILING DATE:
>>> CLASSIFICATION:  536
>>> ATTORNEY/AGENT INFORMATION:
>>> NAME:  Dregler, Ginger R.
>>> REGISTRATION NUMBER:  33,055
>>> REFERENCE/DOCKET NUMBER:  Pl130
>>> TELECOMMUNICATION INFORMATION:
>>> TELEPHONE:  650/225-3216
>>> TELEFAX:  650/952-9881
>>> INFORMATION FOR SEQ ID NO:  4:
>>> SEQUENCE CHARACTERISTICS:
>>> LENGTH:  491 amino acids
>>> TYPE:  Amino acid
>>> TOPOLOGY:  Linear
>>> US-08-933-821-4

```

Query Match	20.9%;	Score 488;	DB 2;	Length 491;
Best Local Similarity	27.0%;	Pred. No. 9.1e-39;		
Matches 129: Conservative	80;	Mismatches 143;	Indels 126;	Gaps 15;

```

QY      46  GRCEGSCQPQLTPTLTITQLP-----RQLSGMEVL-----KEVRT 82
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      42  GKEAKKCATVLPQRTGTPICVNTKGODASTIKDMITRMDLENLKDVLRSQREIDV 101
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      83  LKEAVDSLKSCODCKLQDDHRDPGGNGGNGAETAEDSRVQESQVNLKSELNAKD 142
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```
Db 102 LQLVVDVGDGNIYNEVKLLRKSNN-----MNSRVTQLYMQ---LLHEIIRKRD 146
Qy 143 ---QIOGLOGL- -ETLHLVNNNNIYNDKNVANLTVVNS-----LDGKCKSPSQ 190
Db 147 NSLELSQLENKILNVTTTEMLKMATRYRELEVYASUTDLVNNQSVMTTLEEQCLRFSR 206
Qy 191 EHMOSQP-----VQHL----- 201
Db 207 QDTHVSPPLVQVVPQHIPNSQYTPGLLGCNEIQDPGYPRDMLPPDPLATSPTKSPFKI 266
Qy 202 -----IYKDCSDHYVLGRRSSGAYRTPDHRNSSFEVYCDMETMGGGWTVLQARLD 252
Db 267 PPVTEINEGPFKDCQQAQKAGHSVSGIYMIKPENSNPQMLNCENSILDPGWTIVIQRTD 326
Qy 253 GSTNETREWKDYKAGFNLREFFWLGNDKIHLLTKSKEMILRIDLEDFNGLTLYALYDQF 312
Db 327 GSVNFFRANWENYKKGFGNIDGEYWLGLENIYMLSNQDNKYKLLIELEDWSDKKVYAEYSSF 386
Qy 313 VYANEFLKYRLHIGNYNGTAGDALRESRHYNHDLREFTTPDRDNDRYPSCNCGLYYSSGW 372
Db 387 RLEPESEFYRLGLTYQGNAGDSMMW-----HNGKQFTTLDKDKMY-AGNCAHFHKGW 440
Qy 373 WFDCLSANLNGYY---HOKYKGVNRNGIFWGTWPGINQAPGKYKSFQAKMMIRP 427
Db 441 WYNACAHSNLNGWYRGGHYRSKH-QDGIFWAEYRG-----GSY--SLRAVOMMIKP 489
```

Search completed: February 27, 2001, 12:48:06
Job time: 32 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:35 ; Search time 53.35 Seconds
(without alignments)
964.466 Million cell updates/sec

Title: US-09-442-143-2

Perfect score: 2378

Sequence: 1 MKLANWYLLSSAVLATYGFLL.....GYKSPFKAKMMIRPKHKFP 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2378	100.0	439	4 Q14314	Q14314 homo sapien
2	618.5	26.0	652	5 Q5ND01	Q9ndq1 ciona intes
3	525	22.1	496	11 Q35608	Q35608 mus musculu
4	524.5	22.1	375	6 Q77802	Q77802 bos taurus
5	523.5	22.0	495	4 Q9P2X7	Q9P2X7 homo sapien
6	523	22.0	407	13 Q9PU54	Q9pu54 gallus gall
7	522	22.0	496	4 Q15123	Q15123 homo sapien
8	520	21.9	444	4 Q5NR87	Q9arr7 homo sapien
9	506.5	21.3	312	4 Q08830	Q08830 homo sapien
10	505	21.2	491	4 Q95841	Q08541 homo sapien
11	489	20.6	346	4 Q43827	Q43827 homo sapien
12	486.5	20.5	498	4 Q15389	Q15389 homo sapien
13	485.5	20.4	292	5 Q5U8W8	Q9u8w8 tachypleus
14	485.5	20.4	493	11 Q9R045	Q9r045 mus musculu
15	483.5	20.3	498	11 Q08538	Q08538 mus musculu
16	482.5	20.3	488	13 Q91589	Q91589 xenopus lae
17	481.5	20.2	493	11 Q9J03	Q9j03 rattus norv
18	480.5	20.2	493	4 Q5UKU9	Q9uku9 homo sapien
19	476	20.0	308	5 Q9U8W6	Q9u8w6 tachypleus

20	475	20.0	435	13	O93568	O93568 gallus gall
21	471	19.8	316	5	Q9U8W7	Q9u8w7 tachypleus
22	470.5	19.8	509	11	Q9WVH6	Q9wh6 mus musculu
23	467	19.6	481	6	O18920	O18920 bos taurus
24	452	19.0	334	11	O70165	O70165 mus musculu
25	450	18.9	503	4	Q9Y264	Q9y264 homo sapien
26	438.5	18.4	335	11	Q9WTS8	Q9wts8 rattus norv
27	435.5	18.3	235	6	Q28763	Q28763 papio hamad
28	434.5	18.3	326	6	Q29042	Q29042 sus scrofa
29	428.5	18.0	323	6	Q29041	Q29041 sus scrofa
30	427	18.0	316	6	Q28529	Q28529 mustela put
31	427	18.0	319	4	Q92596	Q92596 homo sapien
32	423	17.8	326	4	Q00602	Q00602 homo sapien
33	423	17.8	1353	13	Q00546	Q00546 gallus gall
34	421.5	17.7	306	11	O70497	O70497 mus musculu
35	421	17.7	712	4	O00531	O00531 homo sapien
36	421	17.7	1358	4	Q92752	Q92752 homo sapien
37	421	17.7	1358	4	Q15568	Q15568 homo sapien
38	420.5	17.7	307	6	Q28703	Q28703 oryctolagus
39	420	17.7	313	4	Q15485	Q15485 homo sapien
40	417.5	17.6	1356	11	O05546	O05546 rattus norv
41	414.5	17.4	299	4	O75836	O75836 homo sapien
42	412.5	17.3	387	5	O18546	O18546 biomphalari
43	405	17.0	440	5	Q9W291	Q9w291 drosophila
44	403.5	17.0	220	6	Q02411	Q02411 sus scrofa
45	403.5	17.0	417	6	Q29038	Q29038 sus scrofa

ALIGNMENTS

RESULT 1
ID Q14314 PRELIMINARY; PRT; 439 AA.
AC Q14314;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytel R.;
RT "Sequence of a human transcript expressed in T-lymphocytes and
encoding a fibrinogen-like protein.";
RL Gene 160:257-262(1995).

Query Match 100.0%; Score 2378; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. le-149;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MKLANWYLLSSAVLATYGFLLVANNTEETKDERAKDVCVRLESRGKCEAGCPQVS 60
|||||

RP SEQUENCE FROM N.A.
RA Yuwaraj S., Liu M., Marsden P., Levy G.;
RT "Cloning and characterization of Hg12: The human counterpart to the
mouse gene Bgl2.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z36531; CAAB5298.1;
DR EMBL: AF104015; AAD10825.1;
DR EMBL: AF104014; AAD10825.1; JOINED.
DR HSSP: P02671; 1FZD.
DR INTERPRO: IPR002181;
DR PFAM: PF00147; fibrinogen_C_1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 439 AA; 50228 MW; DF34656288E49E68 CRC64;

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Db 1 MCLANWYLSAVLATYGVFLVANNETEEIKDERAKDVCPVRLSRKCEPAGCEPQVS 60
QY 61 LPPLTTIQLPKQFSGRIEVEFVQVNLKEIVNSLKKSCQCKIQAADNGDGRNGLLLPSTG 120
Db 61 LPPLTTIQLPKQFSGRIEVEFVQVNLKEIVNSLKKSCQCKIQAADNGDGRNGLLLPSTG 120
QY 121 APEVGDNRVRELESEVKNLSSELKNKAEINVLHGLEKLNLMNMIENYVDSKVANL 180
Db 121 APEVGDNRVRELESEVKNLSSELKNKAEINVLHGLEKLNLMNMIENYVDSKVANL 180
QY 181 TFVNSLDGKSCPSQEQIQSRPVQHLIVKDCSDYIAIGKRSSSETVRYTPDPKNSSEV 240
Db 181 TFVNSLDGKSCPSQEQIQSRPVQHLIVKDCSDYIAIGKRSSSETVRYTPDPKNSSEV 240
QY 241 YCDMETMGCGTQLQARLDGSTNFTRTWQDYKAGFGLNRLREFWLCNDKIHLITKSKEMIL 300
Db 241 YCDMETMGCGTQLQARLDGSTNFTRTWQDYKAGFGLNRLREFWLCNDKIHLITKSKEMIL 300
QY 301 RIDLEDFNGVELYALYDQFYVANEFLYRLHVGNYNGTAGDALRPNKHYNHDLKFFTPPD 360
Db 301 RIDLEDFNGVELYALYDQFYVANEFLYRLHVGNYNGTAGDALRPNKHYNHDLKFFTPPD 360
QY 361 KDNDRVPSGNGLYYSGWFWFACLSANLNGKYHOKYRGVNRGLFWGTWPGVSEAHFPGG 420
Db 361 KDNDRVPSGNGLYYSGWFWFACLSANLNGKYHOKYRGVNRGLFWGTWPGVSEAHFPGG 420
QY 421 YKSFEKAKMIRPKFKP 439
Db 421 YKSFEKAKMIRPKFKP 439

RESULT 2
Q9ND01 PRELIMINARY; PRT; 652 AA.
AC Q9ND01;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN.
GN CI-FIBRN.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;
OC Clonidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RA Hotta K., Takahashi H., Asakura T., Saitoh B., Saitoh N., Satou Y.,
RA Satoh N.;
RT "Characterization of Brachyury downstream notochord genes in the Ciona
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB036849; BAB00626.1; -.
SQ SEQUENCE 652 AA; 73252 MW; A492BA325162F0E0 CRC64;

Query Match 26.0%; Score 618.5; DB 5; Length 652;
Best Local Similarity 43.0%; Pred. No. 3.7e-33;
Matches 120; Conservative 53; Mismatches 91; Indels 15; Gaps 6;

QY 171 NYVDSKVANLT-----FVNSLDG-----KCSKCPSEQIQSRPVQHLIVKDCSDYIAIGK 221
Db 371 NYIYSEGSGVNI RDGYATNETEGIEFTSRILRATNPVQDQGTESLPY-DCAEIYARGV 429
QY 222 RSSETYRYTPDPKNSSEVYCDMETMGCGTQLQARLDGSTNFTRTWQDYKAGFGLNRLRE 281
Db 430 RQSGVYDIRPGTK-VTWTYVYCDMTDGGGWTMLQRRIDGIYFSGKWSKNGFGDINAD 488
QY 282 FWLGNKDIHLIT---KSKEMILRIDLEDFNGVELYALYDQFYVANEFLYRLHVGNYNGT 338
Db 489 HWIGLEKMHILISTNKGRRMELRLNLTDDVDVSHYANTGVFIRSEGNQYLIARKRYGT 548
QY 339 AGDALRPNKHYNHDLKFFTPPDKDNDRVPSGNGLYYSGWFWFACLSANLNGKYHOKY 398
```

```
Db 549 AGDALNGENYNNHQLQPTFTTFRDNDNDGVALGNCGRYRSGWFWFNACFAANLNGNYTGPY 608
QY 399 RGVNRGIFWGTWPGVSEAHFPGGKYSFKEAKMIRPKHF 437
Db 609 KGVQNGIYWGTYKLSDS-TSNSRYSFKYVDMKVRPLNF 646

RESULT 3
O35608 PRELIMINARY; PRT; 496 AA.
ID O35608
AC O35608;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ANGIOPOIETIN 2.
GN ANGPT2 OR AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA MEDLINE-97349327; PubMed=9204896;
RA Maisongier P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziejewski C., Compton D.L., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopietin-2, a natural antagonist for Tie2 that disrupts in vivo
RL Science 277:55-60(1997).
CC -!- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS
CC FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC
CC INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX
CC CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT
CC VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE
CC ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A
CC PERMISSIVE ANGIOGENIC SIGNAL.
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
CC REMODELING.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL: AF004326; AAB63189.1; -.
DR HSSP: P02671; 1FZD.
DR MGD: MGI:1202890; Agpt2.
DR INTERPRO: IPR002181; -.
DR PFAM: PF00147; fibrinogen_C.1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Coiled coil.
FT DOMAIN 55 58 POLY-SER.
FT DOMAIN 159 256 COILED COIL (POTENTIAL).
FT DOMAIN 282 496 FIBRINOGEN BETA/GAMMA.
FT DOMAIN 318 321 POLY-GLY.
SQ SEQUENCE 496 AA; 56616 MW; FA3021FE4E01C410 CRC64;

Query Match 22.1%; Score 525; DB 11; Length 496;
Best Local Similarity 32.9%; Pred. No. 4e-27;
Matches 127; Conservative 65; Mismatches 154; Indels 40; Gaps 9;

QY 61 LPPLTTIQLPKQFSGRIEVEFVQVNLKEIVNSLKKSCQCKIQAADNGDGRNGLLLPSTG 120
Db 142 LTDVEAQLNQITRL-----ELQLQHSISTNKLKQILDQTSSEINKLQKNKSNFL----- 191
QY 121 APEVGDNRVRELESEVKNLSSELKNKAEINVLHGLR-----EKLNLVNMNIENY 172
Db 192 -----EQVLDMEGKHSEQLQSMKEQKQLVLSKQSVIDELEKLVATVNN--SL 243
QY 173 VDSKVANLTFFVNSLDGKSCPSQEQIQSRPVQHLIVKDCSDYIAIGKRSSSETVRYTPD 232
Db 244 LQKQHDLMETVNSLLTMMSSNSPKSSVAIRKEQPTFRDCAEIFKSGLTSGIYTLTFP 303
QY 233 PRNSSFVYCDMETMGCGTQLQARLDGSTNFTRTWQDYKAGFGLNRLREFWLCNDKIHL 292
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Db 304 NSTEIKAYCDMDVGGGWTVIQHRDEGSDVDFQRTWKYKGGFNPGLGTYLWGNFVSQL 363
QY 293 TKSREMILRIDLEDENGVELYALYQFYVANEFYRHLHVGNNGTAGDALRFNKHYND 352
Db 364 TGOHYVLKIQKDWEGNEAHSYDHFYLAGESYRHLTGLTGTAAKISSISQPSGD- 422
QY 353 LKFTTPDKNDRYPSGNCGLYSSGWNFDACLSANLKGYYHQYRGYR-NGIFWGTWP 411
Db 423 ---FSTKSDNDKIC-KCSQMLSGWGFDCGSPSNLNGQYYPQKQNTNFKNGIKYYWK 478
QY 412 GYSAHPCGYKSSFKKAKMIRPKHF 437
Db 479 G-----SGY--SLKATMTMIRPADF 496

RESULT 4
077802 PRELIMINARY; PRT; 375 AA.
ID 077802 Q9TSK0;
AC 077802;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANGIOPOIETIN-2 (FRAGMENT).
GN ANGPT2 OR ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OVARY;
RC MEDLINE=99054348; PubMed=9840613;
RA Goede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
  angiogenesis.";
RL Lab. Invest. 78:1385-1394 (1998).
RN [2]
RP SEQUENCE OF 219-355 FROM N.A.
RX TISSUE-ADRENAL CORTEX;
RC MEDLINE=98451564; PubMed=9776732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
  endothelial cells by cytokines and hypoxia.";
RL Circ. Res. 83:852-859 (1998).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
  MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS
  FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC
  INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX
  CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT
  VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE
  ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A
  PERMISSIVE ANGIOGENIC SIGNAL.
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
  CYCLE. OVEREXPRESSED DURING LUTEOLYSIS. THIS COULD REFLECT THE
  REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
  THE MIDSTAGE CORPUS LUTEUM.
CC -1- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
  THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL: AF094699; AAC62490.1; -.
DR EMBL: AF032924; AAC78285.1; -.
DR HSSP: P02671; 1FZD.
DR INTERPRO: IPR002181; -.
DR PFAM: PF00147; fibrinogen_C.1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
FT NON_TER 1
FT CONFLICT 272 272 S -> L (IN REF. 2).
SQ SEQUENCE 375 AA; 42161 MW; 6F086C4A5C80050A CRC64;

Query Match 22.1%; Score 524.5; DB 6; Length 375;
Best Local Similarity 34.28; Pred. No. 3e-27;

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Matches 136; Conservative 58; Mismatches 139; Indels 65; Gaps 14;
QY 61 LPPLTIQLPQKQFRIEVEFKVONLKEIV--NSLKSCQD-----CKLOADDNGDGPGRG 113
Db 22 LTDVEAQVLNQTPRL-----ELQLEHSLSTNKLKLEQILDQTSISKLQ-----DKNS 69
QY 114 LLLPSTGAPGEVDNRVRELESEVKNLSSELKNAKEEINVLHGR-----LEK-LMLVN 165
Db 70 FL-----EKKVLDMEDKHIVQLRSIKEEKDQLQVLVSKQNSIIELEKQLVTAT 118
QY 166 MNNI-----ENYVDSKVANLTFVNSLDGKCKSPQSOEQIQSRPVQHLIYKDCSDYIAG 220
Db 119 VNNSVLQKQOQHDLMETVNNLLTLMSTSNPYSLLARDEQI-----IFRDCGEAFKSG 170
QY 221 KRSEYRVTPDPKNSSEFYVCDMETMGGWTVLQARLDGSTNFRTRTWODYKAGFGNLR 280
Db 171 LTTSGVYTLTFPNSSTEIKAYCDMETGGGWTVIQRRDEGSDVDFQRTWKYKGGFNP 230
QY 281 EFWLGNDKIHLLTKSEMILRIDLEDENGVELYALYQFYVANEFYRHLHVGNNGTAG 340
Db 231 EHWLGNFEVSVQVTKQRYVLKIHRLDWEGNEAYSLYDHFYLSNEELNYRIHLKGLTGTAG 290
QY 341 DALRFNKHYNHDLKFTTPDKNDRYPSGNCGLYSSGWNFDACLSANLKGYYHQYRG 400
Db 291 KISSISQPGND----FSTKADNDKIC-KCSQMLTGGWGFDCGSPSNLNGMYYPQONT 345
QY 401 VR-NGIFWGTWPCVSEAHPCGYKSSFKKAKMIRPKHF 437
Db 346 NKFNGIKWYWKG-----SGY--SLKATMTMIRPADF 375

RESULT 5
09P2Y7 PRELIMINARY; PRT; 495 AA.
ID 09P2Y7;
AC 09P2Y7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ANGIOPOIETIN-2.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
  Wands J.R.;
RT "Biologic significance of angiopoietin-2 expression in human
  hepatocellular carcinoma.";
RL J. Clin. Invest. 103:341-345 (1999).
DR EMBL: AB009865; BAA95590.1; -.
SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;

Query Match 22.0%; Score 523.5; DB 4; Length 495;
Best Local Similarity 28.1%; Pred. No. 5e-27;
Matches 139; Conservative 76; Mismatches 155; Indels 125; Gaps 16;
QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFEKVN 84
Db 26 MDSIGKKQYQVHGSCSYTFLPEMDNCRSSSPYVSNVAVQROAPLEYDDSDVQRLQVLEN 85
QY 85 LKE-----IVNSLKSCQDCKLOADDNGDGPGRNGLLPSTGAGEVGDN---- 128
Db 86 IMENNTQWLKLENYIQDNMKEMVEIQNAVQN-----QTAVMIEICTNLLNQ 134
QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
Db 135 TABQTRKRLTDVEAQVLNQTPRLQLLEHSLSTNKLKLEQILDQTSISKLSFLERK 194
QY 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLOSIEEKDQLQVLVSKQNSIIELEKKIYVATVNNVSKQOQHDLMET 254

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Db	QY	Db	RESULT	7	015123	PRELIMINARY;	PRT;	496 AA.	
334	---	---	FSTKDTNDKCIC-KCSQMITGGWFWDACGSPNLNGMYIPLRQNNFNKFIKWIYWK	389					
412	GVSEAH	PGGYKSSFK	EAKMIRPKHF	437					
390	G-----	SGY--	SLKAT	TMMIRPADF	407				
015123									
AC	015123								
DT	01-JAN-1998	(T-EMBLrel. 05,	Created)						
DT	01-JAN-1998	(T-EMBLrel. 05,	Last sequence update)						
DT	01-OCT-2000	(T-EMBLrel. 15,	Last annotation update)						
DE	ANGIOPOLETIN-2.								
GN	ANGPT2.								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;				
OC	Mammalia; Eutheria;	Primates;	Catarrhini;	Hominidae;	Homo				

SEQUENCE FROM N.A.
TISSUE=LUNG;
MEDLINE=97349327; PubMed=9204896;
Maisonpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
Radziejewski C., Compton D., McClain J., Aldrich T.H.,
Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
"Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
angiogenesis.";
Science 277:55-60(1997).
-I- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1 (ANG-1). ITS
FUNCTION MAY BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC
INDUCERS, SUCH AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX
CONTACTS MAY INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT
VASCULAR REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE
ENDOTHELIAL CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A
PERMISSIVE ANGIOGENIC SIGNAL.
-I- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
EMBL: AF004327; AB63190.1; -;
HSP; P02671; 1FZD.
MIM: 601922. -;
INTERPRO: IPR002181; -;
PFAM: PF00147; fibrinogen_C. 1.
PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
coiled coil.
55 58 POLY-SER.
DOMAIN 130 256 COILED COIL. (POTENTIAL).
FT DOMAIN

FT	DOMAIN	318	321	POLR-GLY.
SQ	SEQUENCE	496 AA;	56919 MW;	5642A58847A7385C CRC64;
		Query Match	22.0%;	Score 522; DB 4; Length 496;
		Best Local Similarity	27.9%;	Pred. No. 6.3e-27;
		Matches 138; Conservative	74;	Mismatches 159; Indels 124; Gaps
QY	43	LESRKCE--EAGECYQVSLPPL-----	---TQ--LPKQFSRIIEVFKEVQN	84
		: : : : :	: : :	
Db	26	MDSIGKKQYQVHGCSYTFLLPMDNCRSS	SSPYVNAVORDAPLEYDSDVQRQVLEN	85
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
QY	85	LKE-----IVNSLKKSCQCKLQADDNGD	PGRNGLLLPSTGAPGEVGDN----	128
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
Db	86	IMENNTQWLKLENYIQDNMKKEVLIQNAVQ	N-----QTAVMIEIGTNLLNQ	134
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
QY	129	-----RVRELESEV-----	NKLSSELKNAAKEEINVLLHGR-----	LEKL 161
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
Db	135	TAEQTRKLTVDVDAQVLTQTTREQLLEHSL	STNKSEKQILDQTSINKLQDNKSNFLEKK	194
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	
QY	162	NLV-----NMNNIENVDSKVANTTF--	-----V 183	
		: : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : : :	

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Db 195 VLAMEDKHIIQLOSKEEKDQLOVLVSKNSIIIEELEKKIVTATVNVNSVLQKQOHDLMET 254
Qy 184 VNSLDGKSCPSQEQIQRVPQHLIYKDCSDYIAGKRSSETRYVTPDPKNSSEFYVCD 243
Db 255 VNNLLTMMSTNSADPTVAKEEQISFRDCAEVFKSGHTNGIYTLTFPNSTEEIKAYCD 314
Qy 244 METMGGWTVLQARLDGTSNFTWODYKAGFGLNRREFWLGNKDKIHLTKSKEMILRID 303
Db 315 MEAGGGWTTIIRREDGSDVDFORTWKEYKVGFGNPGSEYWLGNFVSQLTNQOQRYVLKI 374
Qy 304 LEDFNGVELYALYDOFYVANEFLKYLHVGNYNGTAGDALRFNKHYNHDLKFFTPDKDN 363
Db 375 LKDWEGNEAYSILYEHFYLSEELNYRIHLKGLGTGAKTSSISQPGND----FSTKGDGN 430
Qy 364 DRYPSCNGLYYSSGWFWFADCLSANLNGKYYHOKYRGVR-NGIFWGTWPGVSEAHPCGYK 422
Db 431 KCIC-KCSOMLTGGWFWFADCLSANLNGMYYPQQRQNTKFNGLIKWYWKG-----SGY- 482
Qy 423 SSFKEAKMMIRPKHF 437
Db 483 -SLKATTMMIRPADF 496

RESULT 8
Q9NR7 PRELIMINARY; PRT; 444 AA.
AC Q9NR7:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ANGIOPOIETIN-2 ISOFORM-1.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
human angiotensin-2."
RL J. Biol. Chem. 275:18550-18556(2000).
DR EMBL; AF187858; AAF76526.1; -.
SQ SEQUENCE 444 AA; 50958 MW; E512409CE73987A1 CRC64;

Query Match 21.9%; Score 520; DB 4; Length 444;
Best Local Similarity 29.6%; Pred. No. 7.4e-27;
Matches 134; Conservative 74; Mismatches 154; Indels 90; Gaps 15;
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Qy 43 LESRGKCE---EAGCEPYQVSLPPL---TIOLPKQFSRIE-----EVFKEVQNLKEIVN 90
Db 26 WDSIGKKQYQVQHGSCSTYFLLPMDNCRSSSPYVSNVAVQADPLEYDDSDVORLQVLEN 85
Qy 91 SLKSCS-----QDCKLQADDNGDPGRNGLLLPSTGAPGEVGNRVRRESEVKNLSS 142
Db 86 IMENNTQMLKVLNQTRELEQ-----LLEHSLSTNKL-EKQILDQTSSEINKLQD 134
Qy 143 -----ELKNAKEEINVHGRLEKLNLVNMMNIENYVDSKVAN----- 179
Db 135 KNSFLEKKVLAMEDKHIIQLOSIKEEKDQLOVLVSKNSI-TEELEKKTIVTAVNNSVLQ 193
Qy 180 -----LTFVNVSLDGKSCPSQEQIQRVPQHLIYKDCSDYIAGKRSSET 226
Db 194 KOQHDLMETVNNLLTMMSTNSAKDPTVAKEEQIS-----FRDCAEVFKSGHTNGI 245
Qy 227 YRVTPDPKNSSEFYVCDMETMGGWTVLQARLDGTSNFTWODYKAGFGLNRREFWLGN 286
Db 246 YTLFPNSTEETKAYCDMEAGGGWTTIIRREDGSDVDFORTWKEYKVGFGNPGSEYWLGN 305
Qy 287 DKIHLLTKSKEMILRIDLEDFNGVELYALYDOFYVANEFLKYLHVGNYNGTAGDALRFN 346
Db 306 EFVSQLTNQOQRYVLKIHLKDWEGNEAYSILYEHFYLSEELNYRIHLKGLGTGAKTSSIS 365
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Qy 347 KHYNHDLKFFTPDKNDNDRYPSCNGLYYSSGWFWFADCLSANLNGKYYHOKYRGVR-NGI 405
Db 366 QPGND----FSTKGDNDKIC-KCSOMLTGGWFWFADCLSANLNGMYYPQQRQNTKFNGLI 420
Qy 406 FWGTWPGVSEAHPCGYKSSFKFAKMMIRPKHF 437
Db 421 KWIYWKG-----SGY--SLKATTMMIRPADF 444

RESULT 9
Q08830 PRELIMINARY; PRT; 312 AA.
ID Q08830:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR.
GN HFREP-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOMA;
RX MEDLINE=93290661; PubMed=8390249;
RA Yamanoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA Hirohashi S.;
RT "Molecular cloning and initial characterization of a novel fibrinogen-
related gene, HFREP-1."
RL Biochem. Biophys. Res. Commun. 193:681-687(1993).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR (PROBABLE).
CC -!- TISSUE SPECIFICITY: OVEREXPRESSED IN HEPATOCELLULAR CARCINOMAS.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL; D14446; BAA03336.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Plasma; Blood coagulation; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 312 FIBRINOGEN-LIKE PROTEIN 1.
FT SIMILAR 70 296 BETA/GAMMA CHAINS OF FIBRINOGEN.
FT DISULFID 83 112 BY SIMILARITY.
FT DISULFID 248 261 BY SIMILARITY.
SQ SEQUENCE 312 AA; 36378 MW; 2330F3D60CD0BBA8 CRC64;
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Query Match 21.3%; Score 506.5; DB 4; Length 312;
Best Local Similarity 36.8%; Pred. No. 3.7e-26;
Matches 118; Conservative 38; Mismatches 108; Indels 57; Gaps 9;

Qy 129 RVRELESEVKNLSSELKNAKEEINVHGRLEKLNLVNMMNIENYVDSKVANLTFVWNSLD 188
Db 36 QVRLLETRVQKQVKKIQLQE-----NEVQFLDKGDETVVD----- 73
Qy 189 GKSCKPSQEQIQRVPQHLIYKDCSDYIAGKRSSETRYVTPDPKNSSEFYVCDMETMG 248
Db 74 -----LGSKRQ-----YADCSEIFNDGYKLSGFYKIKPLQSPAESFYVCDMSD-G 117
Qy 249 GGWTVLQARLDGTSNFTWODYKAGFGLN---RREFWLGNDKIHLTKSKEMILRIDLE 305
Db 118 GGWTVIQRSDGSENFNRGWKDYENGFGNFVQKHGEYWLGNKLNHFLTQEDYTLKIDLA 177
Qy 306 DENGVELYALYDOFYVANEFLKYLHVGNYNGTAGDALRFNKH-----YNHDLKFFTP 359
Db 178 DFEKNSRYAQYKFKVGDENKFNFEINLGEYSGTAGDSLGNHFEVQVWNAHQMKFSTW 237
Qy 360 DKNDNDRYPSCNGLYYSSGWFWFADCLSANLNGKYYHOKYRG-VRNGIFWGTWPGVSEAH 418
Db 238 DRDHDNY-EGNCAEEDQSGWFWNFRCHSANLNGMYYPGTYTAKTDNGIVWYTW----- 288
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QY 419 GGVKSSFKKAKMIRPKHKP 439
Db 289 HGWYSLKSVVMKIRPNDFIP 309

RESULT 10
O95841 PRELIMINARY; PRT; 491 AA.
AC O95841;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE ANGIOPOIETIN Y1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=99148829; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiotensin family
protein, angiotensin-3";
RL FEBS Lett. 443:353-356(1999).
DR EMBL; AF107253; AAD19608.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen.C.1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 491 AA; 56719 MW; 3C4DB8DEF6CF7E99 CRC64;

Query Match 21.2%; Score 505; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 8.3e-26;
Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;

QY 47 GKCEAGCEPYQVSLPLTTIQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKKSCQ 97
Db 42 GK-EAKKCAATFLVPEQRITGPICVTKGQDASTIKDMITRMDLENLKVLSRQKREID 100
QY 98 DCKLQADDNGDPGRNLLLPSTGAPGEVDNRVRELSVKNLSLSEKNAKEEINVLHGR 157
Db 101 VLQLVDVDGN-----IVNEVKLLKRESNMNMSRVTLQYMQ 136
QY 158 L-----EKLNLVNMNNIENVV-----DSKVANLTFVNS-----L 187
Db 137 LLHEITRKRDNLSOLENKLNTVTEMLKMATRYRELVKYASLTDLVNNQSVMTLL 196
QY 188 DGRKSKCPSEQIQSRP-----VQHL----- 208
Db 197 EEQCLRTFSQDTHVSPPLVQVVPQHIPNSQQYTPGLLGGNEIQDPGYPDLMPPPDLA 256
QY 209 -----TYKDCSDYYAIGKRSSEYRVTPDPKNSFFVYCDMETWGG 249
Db 257 TSPTKSPFKIPVPTFINEGPFKDCQAKAEGHSVSGIYMIKPNSENGMPQLWCENSELDPG 316
QY 250 GWTVLQARLDGSTNFTWQDYKAGFNLREFWLGNDKIHLTKSKEMILRIDLEDFNG 309
Db 317 GWTVIQKRTDGSVNFNFWENYKKGFGNIDGEYWLGLNIYMLSNQDNVYKLLIELEWSD 376
QY 310 VELVLYDQFYVANEFLKYRLHVGNYNGTAGDALFRFNKHYNHLKFFTPDKDNDRYPG 369
Db 377 KKYVAEYSSFRLEPESEFYRLRLGTQYQGNAGDSMMW-----HNGKQFTLDRDKDY-AG 430
QY 370 NCGLYSSGWNFDACLSANLNGKYYH--OKYRGV--RNGLFWGTWPGVSAHPGGYKSSPK 427
Db 431 NCAHFHKGWYACAHASHNLNGVYRGHYRKHQDGIFFAEYRG-----GSY--SLRA 482
*QY 428 AKWIRP 434
Db 483 VOMMIKP 489
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RESULT 11
O43827 PRELIMINARY; PRT; 346 AA.
AC O43827;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CD76.
GN DJ647M16.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORNEA;
RA Peek R., van Gelderen B.E., Bruinenberg M., Kijlstra A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Y16132; CAA76078.1; -.
DR EMBL; AL049653; CAB44734.1; -.
DR HSSP; P02671; 1FZD.
DR INTERPRO; IPR002181; -.
DR PFAM; PF00147; fibrinogen.C.1.
SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;

Query Match 20.6%; Score 489; DB 4; Length 346;
Best Local Similarity 36.2%; Pred. No. 6.1e-25;
Matches 117; Conservative 55; Mismatches 113; Indels 38; Gaps 13;

QY 130 VRELSSEVKNLSSEK--NAKEE---INVHGRLE-KLNLVNMNNIENVYDVKVANLTFV 183
Db 49 VKELKAQVANLSLLSELNKKQERDQWVSVVMQVMELESNKRMSRLTDAESKYSMMNQ 108
QY 184 VNSLDGKSKCPSEQIQSRVQHLKYKDCSDYYAIGKRSSEYRVTPDP--KNSSEFVY 241
Db 109 IDIMQLQAQVTVQTSADA-----IY-DCSSLYQKNYRISGVYKLPDDFLGSPLELVF 161
QY 242 CMETMGGGWTVLQARLDGSTNFTWQDYKAGFNLRRREFWLGNDKIHLTKSKEMILR 301
Db 162 CDMEYSGGWTVIQRKSGLVSEFYRDKQYKQFGSIRGDFWLGNEHRLSRQPTR-LR 220
QY 302 IDLEDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAG--DALFRFNKHYNHLKFFTPD 360
Db 221 VEMEDWEGNLRVAYEYSHFVLGNELNSYRLFGLNYTGNVGNDAQY-----HNNTAFSTKD 275
QY 361 KNDRYPSCNCGLYSSGWNFDACLSANLNGKYY-----HOKYRGVNRNGLFWGTWPGVSEA 416
Db 276 KDNQNC-LDKCAQLRKGWYVNCCTDSNLNGVYRLGEHNKH---LDGITWGMHGST-- 329
QY 417 HPGYKSSPKKAKMIRPKHKP 439
Db 330 -----YSLKRVEMKIRPEDFKP 346

RESULT 12
Q15389 PRELIMINARY; PRT; 498 AA.
AC Q15389;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ANGIOPOIETIN-1 (ANG-1).
GN ANGPT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```


192 SLL-----EKKILEME-----GKHKEELDTLKEEKNLOGLVYTPQTYIIQLEKQL 237
 QY 162 NLVNMNNIYVDSKVANLTFVNSLDGKSK-----CPSOEQIQSRPVOHLIYKDCSDYY 217
 Db 238 NRATNN--SVLQKQLELMDTVHNLCTKEGVLLKGGKREEKP-----PRDCADVY 290
 QY 218 AIGKRSETYRV-----TPDPKNSSEFYCYDMETMGGWTVLQARLDGSGTNFTRTWODYKA 273
 Db 291 QAGFNKSGIYTYINNPEPK-----KVFCDNVNNGGWTVIQHREDGSLDFQRGWKEYKM 346
 QY 274 GFGNLRERFWLGNDKIHLTKSKEMILRIDLEDPNGVELYALYDQFVYVANEFLKYRLHVG 333
 Db 347 GFGNPSGEYLLWNEFIFAITSQRYMLRIELMDWEGNRAYSYDIDREFHIGNEKQNYRLYLK 406
 QY 334 NYNCTAGDALRFNKHYNHDLKFFTPDKNDRYPGNCGLVYSSGWWFADACLANSANLNGKY 393
 Db 407 GHTGTACKQSLLIHL-CAD---FSTKQADNDNCMC-KCALMLTGGWWFADACGSNLMGMF 461
 QY 394 YHQ-KYRGVRNGIFWGTWPGVSEAHPGYKSSFKKAKMMIRPKHF 437
 Db 462 YTAGONHGKLGINKWHYFKGPS-----YSLRSTMTMIRPLDF 498

 RESULT 13
 Q9U8W8
 ID Q9U8W8 PRELIMINARY; PRT; 292 AA.
 AC Q9U8W8;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
 DE TACHYLECTIN-5A.
 OS Tachyleptus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyleptus.
 OX NCBI_TaxID=6853;
 RP [1]
 RN SEQUENCE FROM N.A.
 RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
 RA Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.
 RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
 RL Immunity are structurally related to fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
 DR EMBL; AB024737; BAA84188.1; -;
 DR HSSP; P02671; 1FZD.
 DR INTERPRO; IPR002181; -;
 DR PFAM; PF00147; fibrinogen.C:1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 292 AA; 33786 MW; D028DE1E2716F71A CRC64;

 Query Match 20.4%; Score 485.5; DB 5; Length 292;
 Best Local Similarity 36.3%; Pred. No. 8.4e-25;
 Matches 106; Conservative 49; Mismatches 104; Indels 33; Gaps
 QY 159 EKLNLVNMNNIYVDSKVANLTFVNSLDG-KSCSPQEQIQ-----SRPVOHLIY 210
 Db 16 QYGLTSQNK-----LCDVTSSTGLDLSIKVMAHSYKEQLKDKTSEVAQPIVSPDP 69
 QY 211 KDCSDYYAIGKRSEYRYVTPDP--KNSSEFYCYDMETMGGWTVLQAR---LDGSTNFT 265
 Db 70 TDCADILLNGYRSGGYRIWPKSWMTVGTILNVCMDMETDGGWTVIQRGRNGYNPSDYEF 129
 QY 266 RTWQDYKAGGNLRERFWLGNDKIHLTKSKEMILRIDLEDPNGVELYALYDQFVYVANEF 325
 Db 130 KPWNTYKLFGNTEKDFWLGNDRIFFALTQNRNTYMIKDFLDKDKENDTRYAIYQDFWLENE 189
 QY 326 LKYRLHVGNYNGTAGDALRFNKHYNHDLKFFTPDKNDRYPGNCGLVYSSGWWFADACL 385
 Db 190 YLYCLHLIGNYSGDAGNS--FGRNGHN---FSTIDKDHDTHT-HCAQTYIKGWNTYDRCH 243
 QY 386 SANLNGKYHYHQYRGVRNGIFWGTWPGVSEAHPGYKSSFKKAKMMIRPKHF 437
 Db 244 ESNLNGIYLYNGENSVADGTIEWPAWK-----GYHSLUPQVEMKIRPVEF 287

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RESULT 14
Q9R045 PRELIMINARY; PRT; 493 AA.
ID Q9R045
AC Q9R045
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 13, Last annotation update)
DE ANGIOPOIETIN-RELATED PROTEIN-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.O., Koh K.N., Kim H., Uhm C.S., Kwak H.J., Kim N.G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiotensin-
RT related protein. angiotensin-related protein induces endothelial cell
RT sprouting."
RL J. Biol. Chem. 274:26523-26528(1999).
DR EMBL: AF125176; AAD55358.1;
DR HSP: P02671; IZD.
DR INTERPRO: IPR002181;
DR PFAM: PF00147; fibrinogen_C; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 493 AA; 57118 MW; 22885ABEF0746BF2 CRC64;

Query Match 20.4%; Score 485.5; DB 11; Length 493;
Best Local Similarity 30.8%; Pred. No. 1.6e-24;
Matches 117; Conservative 62; Mismatches 128; Indels 73; Gaps 12;

QY 66 IQLPKQSRIEVEKVEV-----QNLKEIVNSLKKSCQDCKLQADDNGDGRNGLLLPSTGA 121
DB :|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
170 LQLASKYKDLKHEKFOHLAMLAHNSQSEVIAQLFEHCQV-----PAARPMPQPPAA 220
QY 122 PGEVGD-----NRVLESEVANKLSSELKNAKEEINVLHGRLEKLNLMNNTNIENYVDSKV 177
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
221 PPRVYQPTYNRI-----INQISTNETQSQDNKLVLPSPSLPTMAL----- 261
QY 178 ANLTFVNSLDGKCKSPCEQIQSRVQHLIKDCSDYIAIGKRSETYRYVTPDPKNSS 237
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
262 -----TSLPSSTDKPSGP-----WRDCLQALEDGHSTSSYLYVKPENTNL 302
QY 238 FEVYCDMETGGGWTVLQARLDGSTNFTRWQDYKAGFNLRRFVLGNDKHLTLTKSKE 297
DB :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
303 MQVWCQDRHDPGGWTVIQRRLDGSVNFERNWETYYKQGFNGIDGYWLGLENIYWLTNQGN 362
QY 298 MILRDLDFNGVELYALYDOFYVANEFLKYRLHVGNYNGTAGDALRFNKNHDLKFTT 357
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
363 YKLLVTMEDWGRKVFAYASFLRPESEYKLRUGRYHGNAGDSFTW-----HNGKQFT 417
QY 358 TPKDNDNRYPSGNCGLYYSSGWWFACLSANLNGKYY---HOKYRGVRNGIFWGTWPGVS 414
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
418 TLRDRHDVY-IGNCAHYKGGWYVYACAHNSLNGWYRGHYSR-YQDGVYWAEEFG--- 473
QY 415 EAHFGGYKSSPEAKMMIRP 434
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
474 ----GSY--SLKKVVMIRP 487

RESULT 15
O08538 PRELIMINARY; PRT; 498 AA.
ID O08538
AC O08538
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE ANGIOPOIETIN-1 (ANG-1).

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GN ANGPT1 OR AGPT
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97134663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisompierre P.C.,
RA Yancopoulos G.D.;
RT "Isolation of angiotensin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning."
RL Cell 87:1161-1169(1996).
CC -!- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING TIE2
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED. MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
DR EMBL: U83509; AAB50558.1;
DR HSP: P02671; IZD.
DR MGD: MGI:108448; Agpt.
DR INTERPRO: IPR002181;
DR PFAM: PF00147; fibrinogen_C; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil.
FT DOMAIN 81 261 COILED COIL (POTENTIAL).
FT DOMAIN 284 498 FIBRINOGEN BETA/GAMMA.
FT CARBOHYD 92 92 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC26D800 CRC64;

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Query Match 20.3%; Score 483.5; DB 11; Length 498;
Best Local Similarity 31.7%; Pred. No. 2.2e-24;
Matches 127; Conservative 62; Mismatches 141; Indels 71; Gaps 14;

QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDGRN 112
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
145 LTDVETQVLNQTSLRLEIQLENSLSTVYKLEQLQQTNEILKTHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVANKLSSELKNAKEEINVLHGR-----LEKMLVN 165
DB :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
192 SLL-----EHLKLEMEGKHKEELTLKEEKENLQGLVSRQTFIIQLEK-QLSR 239
QY 166 MNNIENVDSKVANLTFVNSLDGKCKSK---CPSQSIQSRPVQHLIKDCSDYIAIGK 221
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
240 ATNNLSILOKQLELMDTVHNLVSLCTKEGVLKGGKREEKP-----FRCDADVQAGF 294
QY 222 RSSETYRV-----TPDPKNSSFEVYCDMETMGGGWTVLQARLDGSTNFTRWQDYKAGF 277
DB :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
295 NKSGIITVIFNNMPEK-----KVFNCMDVNGGWTVIQHRDGLSLDFQGMKEVKGFGN 350
QY 278 LRREFVLGNDKHLTLTKSKEMILRIDLEDFNGVELYALYDOFYVANEFLKYRLHVGNYNG 337
DB :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
351 PSGEYWLGNFEIFAITSQRYQYMLRIELMDEGNRAYSQYDRFHIGNEKQNYRLYLKHTG 410
QY 338 TAGDALRFNKNHDLKFTTTPDKDNDNRYPSGNCGLYYSSGWWFACLSANLNGKYYHQ- 396
DB :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
411 TAGKQSSLILH-GAD---FSTKDADNDNCMC-KCALMLTGGWVDFDAGCPNSLNGMFTAG 465

```

QY 397 KYRGVRNGIFWGTWPGVSEAHPGGYKSSFKKAKMMIRPKHF 437
: | || | : | | : | || | |
Db 466 QNHGKLNKGIKWHYFKGPS-----YSLRSTTMMIRPLDF 498

Search completed: February 27, 2001, 12:49:35
Job time: 120 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:35 ; Search time 30.15 Seconds
(without alignments)
497.880 Million cell updates/sec

Title: US-09-442-143-2
Perfect score: 2378
Sequence: 1 MCLANWYLSAVLATYGFLL.....GYKSSFKKMRMPKHKRP 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseq/AA1984.DAT:*

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8: /SIDS1/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseq/AA1988.DAT:*

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19: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	100.0	439	W88235	Human prothrombina
2	1853.5	77.9	432	W88236	Mouse prothrombina
3	524	22.0	314	R65759	Rat hepatic parench
4	522	22.0	496	W01411	Human TIE-2 ligand
5	522	22.0	496	R94605	Human TIE-2 ligand
6	522	22.0	496	W47532	Human TIE-2 ligand
7	522	22.0	496	W178903	Human angiotensin
8	522	22.0	496	W178906	Human angiotensin
9	521.5	21.9	498	W47528	Amino acid sequenc
10	517.5	21.8	499	W47529	Amino acid sequenc
11	506	21.3	312	R94317	Hepatocyte prolife
12	505.5	21.3	312	R94316	Hepatocyte prolife

13	505	21.2	491	20	Y26196	Human zapo3 protei
14	505	21.2	491	20	Y05397	Human TIE ligand N
15	505	21.2	491	21	Y69483	Amino acid sequenc
16	505	21.2	491	21	Y68761	An angiotensin-re
17	504.5	21.2	312	15	R65760	Human hepatic pare
18	500	21.0	491	21	Y44841	Human secreted pro
19	489	20.6	346	20	Y23736	Human AR-1 protein
20	489	20.6	346	20	Y05399	Human TIE ligand N
21	487	20.5	496	19	W47527	Amino acid sequenc
22	487	20.5	497	17	W01410	Human TIE-2 ligand
23	487	20.5	497	17	R94604	Human TIE-2 ligand
24	487	20.5	497	19	W47531	Amino acid sequenc
25	486.5	20.5	498	17	W01409	Human TIE-2 ligand
26	486.5	20.5	498	17	R94603	Human TIE-2 ligand
27	486.5	20.5	498	19	W47530	Amino acid sequenc
28	486.5	20.5	498	21	Y78902	Human angiotensin
29	486.5	20.5	498	21	Y78905	Human angiotensin
30	483.5	20.3	494	19	W47526	Amino acid sequenc
31	481.5	20.2	453	16	R82245	Human fibrinogen g
32	481.5	20.2	453	16	R82246	Human fibrinogen g
33	480.5	20.2	493	20	Y05396	Human TIE ligand N
34	480.5	20.2	493	21	Y70745	PSEQ-3 protein enc
35	480.5	20.2	493	21	Y54999	Human scarface 1 p
36	478.5	20.1	495	21	Y78904	Angiotensin fusio
37	478.5	20.1	495	21	Y78907	Angiotensin fusio
38	470.5	19.8	509	19	W26792	Mouse TIE-2 recept
39	469.5	19.7	509	19	W47533	Amino acid sequenc
40	468	19.7	411	16	R84650	Fibrinogen gamma c
41	461	19.4	491	16	R82243	Human fibrinogen B
42	460.5	19.4	461	21	Y66727	Membrane-bound pro
43	460.5	19.4	509	20	Y23734	TIE ligand-3 (TL3)
44	458.5	19.3	454	16	R84551	Partial human fibr
45	458	19.3	386	20	Y59881	Human normal uteru

ALIGNMENTS

RESULT 1
W88235
ID W88235 standard; Protein; 439 AA.
XX
AC W88235;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human prothrombinase Fg12 protein.
XX
KW Prothrombinase; hfg12; Fg12; human; immune coagulation; antibody;
KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
KW gastrointestinal disease; foetal loss; therapy; vaccine.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Modified-site 179..183
FT Modified-site /label= Asn is N-glycosylated
FT Modified-site 235..238
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 262..265
FT Modified-site /note= "Asn is N-glycosylated"
FT Modified-site 336..337
FT Modified-site /note= "Asn is N-glycosylated"
FT Domain 213..439
FT Peptide /note= "fibrinogen related domain"
FT Peptide 364..378
FT Peptide /note= "epitope (Claim 4)"
XX
WO9851335-A1.
XX
PD 19-NOV-1998.
XX
PF 15-MAY-1998; 98WO-CA00475.

applied

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XX PR 10-OCT-1997; 97US-0061684.
XX PR 15-MAY-1997; 97US-0046537.
XX PA (LEVY/) LEVY G.
XX PI Levy G;
XX XX
DR WPI; 1999-059687/05.
DR N-PSDB; V84139.
XX XX
XX PT Modulating immune coagulation - by using Fgl2 antibodies and
XX PT compounds, used to treat conditions including graft rejection and
XX PT foetal loss
XX XX
PS Claim 8; Page 66-67; 105pp; English.
XX XX
CC This is the amino acid sequence of human prothrombinase Fgl2, as
CC predicted from hfgl2 DNA (see V84139). Fgl2 is a 70 kDa
CC transmembrane serine protease that has immune procoagulant activity.
CC The invention provides a method for inhibiting immune coagulation by
CC inhibiting the activity or expression of Fgl2. The method can be
CC used in vivo to treat a condition which requires a reduction in
CC immune coagulation such as bacterial and viral infections, cancer,
CC glomerulonephritis, a number of gastrointestinal diseases,
CC allograft and xenograft rejection and foetal loss. An Fgl2-specific
CC antibody, an Fgl2 antisense oligonucleotide, or a substance that
CC affects prothrombinase activity of a Fgl2 protein may be used to
CC treat a condition requiring a reduction in procoagulant activity.
CC A vaccine containing an Fgl2 protein or peptide is used for
CC prevention of graft rejection or foetal loss (claimed).
XX XX
SQ Sequence 439 AA;

Query Match 100.0%; Score 2378; DB 20; Length 439;
Best Local Similarity 100.0%; Pred. No. 8.2e-206;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M KLANWYLSAVLATYGFVIVANNETEIKDERAKDVCVPRLESRGKCEEGECPYQVS 60
Db 1 m klanwywlsavlatygfvlvannetei kderakdvcvprlesrgkceegecpyqvs 60

QY 61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRNGLLPSTG 120
Db 61 lppltiqlpkqfsrieefvkevnleivns lkkscdqcklqaddngdpgrngllpstg 120

QY 121 APGEVGDNRVRELESEVNKLSSELKNAKEEINVLHGRLEKLNLMNNNTENYVDSKVANL 180
Db 121 apgevgdnrvrelesevnklselknakee invlhgrlekl nlmnnntenyvdskvanl 180

QY 181 TFVNSLDGKSKCPSQEQIQSRPQHLIYKDCSDYAYAGKSSERYTYTPDPKNSFEV 240
Db 181 tfvnsldgkscpsqeqiqsrpqhliykdc sdyayagksserytytpdpknsfev 240

QY 241 YCDMETMGGVTVLQARLDGSTNFTRTWODYKAGFCNLRREFWLGNDKIHLLTKKSEMIL 300
Db 241 ycdmetmggvtvlqarldgstnft rtwodykagfcnlrrefwlgndk ihlltksemil 300

QY 301 RIDLEDNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALRFNKHYNHDLKFTTTPD 360
Db 301 ridledngvelyalydqfyvane flkyrlhvgnyngtagdalrfnkh ynhdltkfttpd 360

QY 361 KDNDRYPGSGCLYYSYSSGWWFDACISANLNGKYHOKYGVNRGIFWGTWPGVSEAHPGG 420
Db 361 kdndrypsgclyysyssgwwfdacis anlngkyhokygvnr gifwtwpgvseahpgg 420

QY 421 YKSSFKEAKMMIRPKHFKP 439
Db 421 ykssfkeakmmirpkhfkp 439
```

RESULT 2

```
W88236
ID W88236 standard; Protein; 432 AA.
XX AC W88236;
XX DT 15-MAR-1999 (first entry)
XX DE Mouse prothrombinase Fgl2 protein.
XX XX
KW Prothrombinase; Fgl2; mouse; immune coagulation; antibody;
KW inhibitor; infection; graft rejection; glomerulonephritis; cancer;
KW gastrointestinal disease; foetal loss; therapy; vaccine.
XX OS Mus sp.
XX XX
FH Key Location/Qualifiers
FT Modified-site 172..174
FT /label= Asn is N-glycosylated
FT Modified-site 228..231
FT /note= "Asn is N-glycosylated"
FT Modified-site 256..259
FT /note= "Asn is N-glycosylated"
FT Modified-site 323..325
FT /note= "Asn is N-glycosylated"
FT Domain 213..439
FT /note= "fibrinogen related domain"
XX XX
XX W09851335-A1.
XX 19-NOV-1998.
XX 15-MAY-1998; 98WO-CA00475.
XX 10-OCT-1997; 97US-0061684.
XX 15-MAY-1997; 97US-0046537.
XX (LEVY/) LEVY G.
XX Levy G;
XX WPI; 1999-059687/05.
XX N-PSDB; V84140.
XX XX
XX Modulating immune coagulation - by using Fgl2 antibodies and
XX compounds, used to treat conditions including graft rejection and
XX foetal loss
XX XX
PS Claim 8; Page 70-71; 105pp; English.
XX XX
CC This is the amino acid sequence of mouse prothrombinase Fgl2, as
CC predicted from fgl2 DNA (see V84140). Fgl2 is a 70 kDa
CC transmembrane serine protease that has immune procoagulant activity.
CC The human Fgl2 amino acid sequence is given in W88236. The
CC invention provides a method for inhibiting immune coagulation by
CC inhibiting the activity or expression of Fgl2. The method can be
CC used in vivo to treat a condition which requires a reduction in
CC immune coagulation such as bacterial and viral infections, cancer,
CC glomerulonephritis, a number of gastrointestinal diseases,
CC allograft and xenograft rejection and foetal loss. An Fgl2-specific
CC antibody, an Fgl2 antisense oligonucleotide, or a substance that
CC affects prothrombinase activity of a Fgl2 protein may be used to
CC treat a condition requiring a reduction in procoagulant activity.
CC A vaccine containing an Fgl2 protein or peptide is used for
CC prevention of graft rejection or foetal loss (claimed).
XX XX
SQ Sequence 432 AA;
```

```
Query Match 77.9%; Score 1853.5; DB 20; Length 432;
Best Local Similarity 77.7%; Pred. No. 1.4e-158;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

QY 1 M KLANWYLSAVLATYGFVIVANNETEIKDERAKDVCVPRLESRGKCEEGECPYQVS 60
```

```

CC      The protein or the N-terminal peptide (R65758) may be used in the
CC-      diagnosis and treatment of liver diseases, such as liver cancer and
CC      cirrhosis.
CC      xx
SQ      Sequence          314 AA;

      Query Match          22.0%; Score 524; DB 15; Length 314;
      Best Local Similarity 37.6%; Pred. No. 4.3e-39;
      Matches 124; Conservative 46; Mismatches 104; Indels 56; Gaps 13;

Qy      125 VGD--NRVRE---LSEYVKLSSELKNAKEET--NYLHGRLLEKLNLVNMMNTIENVYDSKVAN 179
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      23 lgnclnqeqvrlraqvrlqetrkvqqvyaqlhxx---evqfldrgqdsfid----- 75

Qy      180 LTFVYVNSLDGRKSCKCPSEQEQIQSRPVQHLIYKDCSDYYAIGKKSSEYRYVTPPKNSSFE 239
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      76 -----lggk----- --rh--yadcsejyngdfkhsfykikpqlslaefs 111

Qy      240 VYCDMETWGGGWTVLQARLDGSTNFTFTWQDYKAGFNL---RREFWLGNDKTHLLTKSK 296
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      112 vycdmsd--ggsgwtvlgrrsdgsenfnrgwnydgfnfvqsgngeywlgnknlltmqg 170

Qy      297 EMILRIDLEDPNGVELYALDOFVYVANEFLKYRLHVNGNYGTAGDALRFNKH-----YN 350
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      171 dytkidltdeksrfaeqekfvkgdeksfyelnieygsctagdsisgfhfpevqvwaa 230

Qy      351 HDLFFFTTPDKNDRYPSGNGCLYSSGWWFDACLSANLKGKYYHQKYRG--VRNGIFWGT 409
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      231 hntmkfstfrdrndny--nqncaeaeegsqwvfnrcrchanlnqvyvqgqvraetdngvwyvt 289

```

QY	410	WPGVSEAHPGGYKSSFEAKMMIRPKHKFP	439
	1:		
Db	290	w-----fgwysllksvvmkirpsdfip	311
RESULT	4		
W01411			
XX	W01411	standard; Protein; 496 AA.	
XX	AC	W01411;	
XX	XX		
XX	DT	11-FEB-1997 (first entry)	
XX	XX		
DE	DE	Human TIE-2 ligand 2.	
XX	XX		
KW	KW	TIE-2 ligand 2; tyrosine kinase with Ig and EGF homology domain;	
KW	KW	receptor; antagonist; neovascularisation; wound healing; ischaemia;	
KW	KW	leukopaenia; thrombocytopaenia; anaemia; angiogenesis; tumour;	
KW	KW	atherosclerosis; inflammation; diagnosis; therapy.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	W09631598-A1.	
XX	XX		
PD	PD	10-OCT-1996.	
XX	XX		
PF	PF	05-APR-1996; 96WO-US04806.	
XX	XX		
PR	PR	06-OCT-1995; 95WO-US12935.	
PR	PR	06-APR-1995; 95US-0418595.	
XX	XX		
PA	PA	(REGE-) REGENERON PHARM INC.	
XX	XX		
PI	PI	Aldrich TH, Bruno J, Davis S, Goldfarb M, Jones PF;	
PI	PI	Maisonpierre PC, Radziejewski C, Yancopoulos GD;	
XX	XX		
DR	DR	WPI; 1996-465021/46.	
DR	DR	N-PSDB; T44321.	
XX	XX		
PT	PT	TIE-2 agonists and antagonists and related DNA - useful for	
XX	XX	promoting or blocking neovascularisation, etc	

[illegible]

```

Db 375 lkdwegneasylyehfylsseelnryihlkgltgtagkissisqpgnd----fstkdgdnd 430
QY 364 DRYPSGNCGLIYSSGWFDAACLSANLNGKYHQQYRGVR-NGIFWGTWPGVSEAHPPGYK 422
Db 431 dkci-c-kcsqmlggwfdacgpsnngmyppqrqntnkfngikwywkg-----sgy- 482
QY 423 SSFKEAKMMIRPKHF 437
Db 483 -slkattmmirpadf 496

RESULT 6
W47532
ID W47532 standard; Protein; 496 AA.
XX
AC W47532;
XX
DT 09-SEP-1998 (first entry)
XX
DE Human TIE-2 ligand 2 from clone pBluescript KS.
XX
KW Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation;
XX tumour; human.
XX
OS Homo sapiens.
XX
PN WO9805779-Al.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13557.
XX
PR 25-OCT-1996; 96US-0740223.
XX
PR 02-AUG-1996; 96US-0022999.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Yancopoulos GD;
XX
XX WPI; 1998-145615/13.
DR N-PSDB; V18619.
XX
XX Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing
XX
PS Example 8; Fig 6; 202pp; English.
XX
XX This is the amino acid sequence of the human TIE-2 ligand 2,
CC used in the method of the invention, involving the production
CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
CC and host cells used in the method of the invention are useful for
CC the recombinant production of the ligands. The ligands, etc. are
CC useful for blocking blood vessel growth, promoting neovascularisation,
CC promoting the growth or differentiation of a cell expressing the TIE
CC receptor, blocking the growth or differentiation of a cell expressing
CC the TIE receptor and for attenuating or preventing tumour growth in
CC a human.
XX
SQ Sequence 496 AA;

```

Query Match 22.0%; Score 522; DB 19; Length 496;
 Best Local Similarity 27.9%; Pred. No. 1.3e-38;
 Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

```

QY 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEVEFKVQN 84
Db 26 mdsigkkgvqngsgcsytlfpemdncrsssspyvsnvgrdpleyddsqrqlgven 85
QY 85 LKE-----TVNSLKKSCQDCKLQADNDGDPGRNGLLLPSTGAPGEVDN--- 128
Db 86 inenntqwmklienylqdmnkemveiqnavqn-----qtavmiegtlnlq 134

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QY 129 -----RVRELESEV-----NKLSELKNAKEEINVLHGR---LEKL 161
Db 135 taeqtrkltdveaqvlnqtrlelqllehs1stnkleqilqdtseinklqdknsflekk 194
QY 162 NLV-----NMMNIENYVDSKVANLTF-----V 183
Db 195 vlamedkhiqlqsikeekdqivskqnsleekikivtatvnnsvlqkqhdmet 254
QY 184 VNSLDGKCKSPSQEQIQSRPVQHLLYKDCSDYATGKRSETYRYTPDPKNSSEVYCD 243
Db 255 vnnlltmmstnsakdptvakeeqisfrdaevfsghtngiytltfpnsteelkaycd 314
QY 244 METMGGWTVLQARLDGSGTNFTRTWDYKAGFGNLRREFWLGNDKIHLTKSEMILRID 303
Db 315 meaggvgwtiqrredsgvdfqrtekykvfgnpsgeywlgnfvsqlnqgryvlkih 374
QY 304 LEDFNGVELYALYDQFYVANEFKYRLHVGNVNTAGDALRNFKNHYNHDLKFFTTDKDN 363
Db 375 lkdwegneasylyehfylsseelnryihlkgltgtagkissisqpgnd----fstkdgdnd 430
QY 364 DRYPSGNCGLIYSSGWFDAACLSANLNGKYHQQYRGVR-NGIFWGTWPGVSEAHPPGYK 422
Db 431 dkci-c-kcsqmlggwfdacgpsnngmyppqrqntnkfngikwywkg-----sgy- 482
QY 423 SSFKEAKMMIRPKHF 437
Db 483 -slkattmmirpadf 496

RESULT 7
Y78903
ID Y78903 standard; Protein; 496 AA.
XX
AC Y78903;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human angiotensin-2 amino acid sequence.
XX
KW Angiotensin-2; Ang-2; vascular endothelial growth factor; tumour;
KW vascularisation; angiogenesis; blood vessel maturation; malignant;
KW benign; binding ligand; cancer; aminophospholipid.
XX
OS Homo sapiens.
XX
PN WO200002587-Al.
XX
PD 20-JAN-2000.
XX
PF 12-JUL-1999; 99WO-US15668.
XX
PR 13-JUL-1998; 98US-0092589.
XX
PR 02-DEC-1998; 98US-0110600.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Thorpe PE, Ran S;
XX
DR WPI; 2000-182177/16.
DR N-PSDB; 292213.
XX
XX Binding ligand for aminophospholipid used in the treatment of
PT vascularised tumours, comprises targeting component and therapeutic
PT agent
XX
XX Disclosure; Page 257-259; 267pp; English.
XX
XX This sequence represents the human angiotensin-2 (Ang-2) amino acid
CC sequence. Ang-2 is a naturally occurring angiogenesis antagonist when
CC vascular endothelial growth factor (VEGF) levels are low, and generally
CC counteracts the blood vessel maturation and stability mediated by Ang-1.
CC Ang-1 is a naturally occurring angiogenesis agonist, and is a maturation
CC or stabilisation factor, converting immature vessels to mature vessels.

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Db 431 dkci-cscqmtgwwfdacgpnslngmyppqrqntkngikwywkg-----sgy- 482
 QY 423 SSFKEAKMMIRPKHF 437
 Db 483 -slkattmmirpadf 496
 RESULT 9
 W47528
 ID W47528 standard; Protein; 498 AA.
 XX
 AC W47528;
 XX
 DT 09-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of chimeric TIE ligand IN1C2F (chimera 1).
 XX
 KW Chimeric TIE ligand IN1C2F; TIE-2 ligand; neovascularisation;
 tumour; human.
 XX
 OS Homo sapiens.
 XX
 PN W09805779-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-US13557.
 XX
 PR 25-OCT-1996; 96US-0740223.
 PR 02-AUG-1996; 96US-0022999.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Davis S, Yancopoulos GD;
 XX
 DR WPI; 1998-145615/13.
 DR N-PSDB; V18615.
 XX
 PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
 PT healing
 XX
 PS Claim 20; Fig 24; 202pp; English.
 XX
 CC This is the amino acid sequence of the chimeric TIE ligand IN1C2F,
 CC used in the method of the invention, involving the production
 CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
 CC and host cells used in the method of the invention are useful for
 CC the recombinant production of the ligands. The ligands, etc. are
 CC useful for blocking blood vessel growth, promoting neovascularisation,
 CC promoting the growth or differentiation of a cell expressing the TIE
 CC receptor, blocking the growth or differentiation of a cell expressing
 CC the TIE receptor and for attenuating or preventing tumour growth in
 CC a human.
 XX
 SQ Sequence 498 AA;
 Query Match 21.9%; Score 521.5; DB 19; Length 498;
 Best Local Similarity 32.7%; Pred. No. 1.5e-38;
 Matches 131; Conservative 61; Mismatches 138; Indels 71; Gaps 14;
 QY 61 LPPLTLPKQFSRIE-----EVFKEVONLKEIVNSLKKSCQDKLQADDNGDPGRN 112
 Db 145 ldtvetqlngtrleiglenslstykqlqllqtnfeikhe-----kn 191
 QY 113 GLLLPSTGAPGEVDNRVRELSVNNKLSLKNKAEINVLHG-----RLEK-L 161
 Db 192 sl1-----ehkilene---ghkkeltdtkkeenlglvtrqtyiigelekql 237
 QY 162 NLVNMMNNIENVDSKVANLTFVNSLKGKSK-----CPSQBIQSRPVQHLIYKDCSDYY 217
 Db 238 nrattnn--svlqkqqlmdtvtlnlctkegvlkkgkreekp-----frdcaevf 290

QY 218 ATGKRSETRYRTPDPKNSSEFVYCDMERNMGGWTVLQARLDGSTNFTRTWQDYKAGFGN 277
 Db 291 ksghtngiytltposteeikaycdmeaggggtliqirredgsdvdfrtwkeykvvgfn 350
 QY 278 LRREFWLGNDKIHLLTKSEMILRIDLEDPNGVELYALYDQFYVANEFLKYRLHVGNYNG 337
 Db 351 psgeywlgnfsvqltnqgrvylkhlkdwegneayslyedfylsseeelnryrlhkgltg 410
 QY 338 TAGDALRFNKHVNDLKFETTPDKDNDRVPSPGNCGLYSSGWMFDCLSANLKGKYYHOK 397
 Db 411 tagkissisqpgnd----fstkdgdndkclc-kcsgmltggwwfdacgpnslngmyppqr 465
 QY 398 YRGVR-NGIFWGTWPGVSEAHPGGYKSSPKAKMMIRPKHF 437
 Db 466 qntnkngikwywkg-----sgy--slkattmmirpadf 498
 RESULT 10
 W47529
 ID W47529 standard; Protein; 499 AA.
 XX
 AC W47529;
 XX
 DT 09-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of chimeric TIE ligand IN2C2F (chimera 3).
 XX
 KW Chimeric TIE ligand IN2C2F; TIE-2 ligand; neovascularisation;
 KW tumour; human.
 XX
 OS Homo sapiens.
 XX
 PN W09805779-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-US13557.
 PR 25-OCT-1996; 96US-0740223.
 PR 02-AUG-1996; 96US-0022999.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Davis S, Yancopoulos GD;
 XX
 DR WPI; 1998-145615/13.
 DR N-PSDB; V18616.
 XX
 PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
 PT healing
 XX
 PS Claim 20; Fig 26; 202pp; English.
 XX
 CC This is the amino acid sequence of the chimeric TIE ligand IN2C2F,
 CC used in the method of the invention, involving the production
 CC of TIE-2 ligands which promote healing. The nucleic acids, vectors
 CC and host cells used in the method of the invention are useful for
 CC the recombinant production of the ligands. The ligands, etc. are
 CC useful for blocking blood vessel growth, promoting neovascularisation,
 CC promoting the growth or differentiation of a cell expressing the TIE
 CC receptor, blocking the growth or differentiation of a cell expressing
 CC the TIE receptor and for attenuating or preventing tumour growth in
 CC a human.
 XX
 SQ Sequence 499 AA;

Query Match 21.8%; Score 517.5; DB 19; Length 499;
 Best Local Similarity 28.1%; Pred. No. 3.4e-38;
 Matches 133; Conservative 73; Mismatches 166; Indels 101; Gaps 13;
 QY 44 ESRGKCEAGECPYQVSL-----PPLTLPKQFSRIEVEFKEVONLKEIVNSLKK 94

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Db 49 ehgncresttdqyntalnqrdrphvdpddsvqrlqvlennime--nntqwlmklenyiqd 106
Qy 95 SCQDCKLQADDNGDCRNGLLLPSTGAPGEVGN-----RVRELESEV----- 137
Db 107 nmkkemveiqqnnavqngtavmi-----eigtlnllnqtaeqtrkitdveaqvlnqtrtl 159
Qy 138 -----NKLSELKNAEEINVLHGR---LEKLNLV----- 164
Db 160 elqllehslstnklekqildtseinklqdknsflekkvllamedkhiilqlsqikeekdql 219
Qy 165 -----NMNIENKVDKSNANLAF-----VNSLDGKCKSCPSQEQIQSRPV 205
Db 220 qvlsvkqnsiieelekkivtatvnnsvlqkqhdlnmetvnlltmmstnsakdptvake 279
Qy 206 QHLIYKDCSDYYAIGKRSEYRTVPDPKNSSEFYVCDMETMGGMVTLQARLDGSGTNFT 265
Db 280 eqisfrdcaevfksghtngtiyltfnsteeikaycdmeagggwtliqrredgsvdfq 339
Qy 266 RTWQDYKAGFNLRRFVWLGNDKIHLLTKSEKILRIDLEDFNGVELYALYDOFYVANEF 325
Db 340 rtwkeykvfgnpsgeywnfnefvsqtnqgryvllkhlkdwegneayslyehfyssee 399
Qy 326 LKYLHVGNNGTAGDALRNFKNHNDLKFFTPDKDNDRYPSGNCGLYSSGWWFQACL 385
Db 400 lnyrihikgltagkissiqpnd-----fstkdgdndkcic-kcsqmltggwffdaog 454
Qy 386 SANLNGKYYHOKYRGVR-NGIFWGTWPGVSEAHHPGGYKSFKEAKMIRPKHF 437
Db 455 psnlmgmyyprqntknfngikwywkg-----sgy--slkattmmirpadf 499

RESULT 11
R94317
ID R94317 standard; Protein; 312 AA.
XX
AC R94317;
XX
DT 05-NOV-1996 (first entry)
DE Hepatocyte proliferation substance HP-041V.
XX
KW Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter;
KW chinese hamster ovary cell; CHO; hepatitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22 /note= "signal peptide"
FT Protein 23..312 /note= "mature protein"
XX
PN WO9609383-AL.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-JP01904.
XX
PR 22-SEP-1994; 94JP-0228234.
XX
PA (TAIS ) TAISHO PHARM CO LTD.
XX
PI Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;
XX
DR WPI; 1996-188445/19.
DR N-PSDB; T13397.
XX
PT Vector for expression of hepatocyte proliferation substance - in
PT eukaryotic cells, used as diagnostic reagent for hepatitis and for
XX basic research on in vitro liver cell cultures
XX
PS Example 3; Page 28-29; 44pp; Japanese.
XX

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CC This is the amino acid sequence of a variant human hepatocyte
CC proliferation substance (HPS). The variant differs from the sequence
CC encoded by T13396 at pos. 214: A to G change and pos. 314: T to C. These
CC changes alter the amino acid residues at pos. 50 of the mature protein:
CC ile to Val and pos. 83: Leu to Pro. The gene was isolated from a
CC lambda-gt10 human cDNA library using the sequence T13396 as a probe.
CC The human gene was cloned in plasmid pSCL to produce plasmid pSVLH which
CC was subsequently recombined to produce plasmid pCDLH-dhfr in which the
CC HPS gene is under control of the SR-alpha promoter. This plasmid is
CC transformed into CHO cells to express the HPS protein. The HPS protein
CC can be used to diagnose hepatitis.
XX
SQ Sequence 312 AA;

Query Match 21.3%; Score 506; DB 17; Length 312;
Best Local Similarity 44.6%; Pred. No. 1.8e-37;
Matches 107; Conservative 25; Mismatches 88; Indels 20; Gaps 6;

Qy 210 YKDCSDYYAIGKRSEYRTVPDPKNSSEFYVCDMETMGGMVTLQARLDGSGTNFTWQ 269
Db 80 yadceifndgkylsgfykikplqspaeafsvydcmsd-gggwtvqirsdgsenfngwk 138
Qy 270 DYKAGFNL---RREFWLGNDKIHLLTKSEKILRIDLEDFNGVELYALYDOFYVANEF 326
Db 139 dyengfgnfvqkhegywlgknknlhlttqedytkidladfeknsryaqyknfkvgdekn 198
Qy 327 KYRLHVGNNGTAGDALRNFKNH-----YNHDLKFFTPDKDNDRYPSGNCGLYSSGWW 380
Db 199 fyelnigeysgtagdsiagnfhpeqvwasqrmkfstwdrdhny-egnceaedqsgww 257
Qy 381 FDACLSANLNGKYYHOKYRG-VRNGIFWGTWPGVSEAHHPGGYKSFKEAKMIRPKHF 439
Db 258 fnrchsanlngvyygpytaktngivwtw-----hgwwylsksvvmkripndfip 309

RESULT 12
R94316
ID R94316 standard; Protein; 312 AA.
XX
AC R94316;
XX
DT 05-NOV-1996 (first entry)
DE Hepatocyte proliferation substance HP-041.
XX
KW Human hepatocyte proliferation substance; rat; probe; SR-alpha promoter;
KW chinese hamster ovary cell; CHO; hepatitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..22 /note= "signal peptide"
FT Protein 23..312 /note= "mature protein"
XX
PN WO9609383-AL.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-JP01904.
XX
PR 22-SEP-1994; 94JP-0228234.
XX
PA (TAIS ) TAISHO PHARM CO LTD.
XX
PI Hanada K, Hara H, Matsuki Y, Shindo S, Yoshimura H;
XX
DR WPI; 1996-188445/19.
DR N-PSDB; T13396.
XX
PT Vector for expression of hepatocyte proliferation substance - in

```

FT	Peptide	93..98
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

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Db 101 vlqlvvdvgn-----ivnevkllrkesnmnsrvtqlmq 136
 Qy 158 L-----EKLNVNMMNIENV-----DSKVANLTFVNS-----L 187
 Db 137 llheirkrdslelsqlenklnvttemlkmnatryrelekvysitdlvnnqsvmitll 196
 Qy 188 DKCKSKCPSEQIQSRP-----VQHL----- 208
 Db 197 eeqclrifsgdthvspplvqvpphpnsgqytpgllgngneiqrdpgyprdlmppedla 256
 Qy 209 -----IYKDCSDYYAIGKRSSSEYRVTTPPKNSSFEVYCDMETMGG 249
 Db 257 tsptksfpkippvtfinepfkdcqakeaghsvglmkipensngpmqlwcensldpg 316
 Qy 250 GWTVLQARLDGSTNFTWQDYKAGFNLREFWLGNDXIHLLTKSEKEMILRIDLEDENG 309
 Db 317 gwtvlgkrtgdsgvnfrwnykgfgnidgelywlglenlymnsqndnykllieledwsd 376
 Qy 310 VELYALYDOFYVANEFLKYLRLHVGNYNGTAGDALRFRNKHYNHDLKFFTPDKNDRYPSG 369
 Db 377 kkvyaeysfrlepeseefyrlrlgtvggnagdsmmw-----hngkqftldrdkdm- 430
 Qy 370 NCGLYSSGWFFDACLSANLNGKYH-QKRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427
 Db 431 ncahfkggwwynacahsnlmgvyrghyrskhgdfwaeyrg-----gsy--slra 482
 Qy 428 AKMMIRP 434
 Db 483 vqmmikp 489

RESULT 14

Y05397
 ID Y05397 standard; Protein; 491 AA.

XX Y05397;

AC Y05397;

XX Y05397;

DT 01-JUL-1999 (first entry)

DE Human TIE ligand NL5 protein sequence.

XX Human TIE ligand; NL4; NL5; NL8; Ig homology domain; angiogenesis;
 KW EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
 KW early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
 KW endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
 KW vasculogenesis; detection; diagnosis; therapy.

XX Homo sapiens.

XX WO9915653-A2.

PN 01-APR-1999.

PD 14-SEP-1998; 98WO-US19093.

XX 29-OCT-1997; 97US-0960507.

PR 19-SEP-1997; 97US-0933821.

XX (GETH) GENENTECH INC.

PA Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;

PI Hillan K, Roy M, Schwall R, Tumas D;

XX WPI; 1999-263480/22.

DR N-PSDB; X36342.

XX New isolated TIE ligand homologs for, e.g. developing products for

PT treatment of tumors

PS Claim 8; Fig 5; 132pp; English.

XX This sequence is the human tyrosine kinase containing Ig and EGF

CC homology domains (TIE) ligand of the invention, designated NL5.

CC The TIE receptors are receptor tyrosine kinases which are expressed in
 CC vascular endothelial cells and early haemopoietic cells. The TIE
 CC receptors are believed to be actively involved in angiogenesis, and may
 CC play a role in haemopoiesis as well. The TIE ligand homologs can promote
 CC the survival and/or growth and/or differentiation of TIE receptor
 CC expressing cells. They can be used for promoting neovascularisation in
 CC wound healing and for promoting angiogenic processes, such as for
 CC inducing collateral vascularisation in an ischaemic heart or limb, or for
 CC promoting bone development and/or maturation and/or growth in a patient
 CC or muscle growth and development. The TIE ligand homologs and antibodies
 CC can inhibit the growth of endothelial cells and induce apoptosis of
 CC cells, particularly tumour cells. They can inhibit vasculogenesis,
 CC particularly the vascularisation of tumour cells. The antibodies can also
 CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,
 CC NL8 or NL4 polypeptide is amplified. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic
 CC animals.

XX Sequence 491 AA;

SQ Query Match 21.2%; Score 505; DB 20; Length 491;

Best Local Similarity 26.9%; Pred. No. 4.4e-37;

Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;

QY 47 GKCEAGECPYQVSLPPLTTQLP-----KQFSRIEEVF--KEVQNLKEIVNSLKSCQ 97

Db 42 gk-eeakkcaytfilvpegritgpcvntkqgdastikdmtrmdlenlkdvlsrqkreid 100

QY 98 DCKLOADDNGDPGRNLLLPSTGAPGEVGDNRVRELSEVKNLSSELKNAKEEINVLHGR 157

Db 101 vlqlvvdvgn-----ivnevkllrkesnmnsrvtqlmq 136

QY 158 L-----EKLNVNMMNIENV-----DSKVANLTFVNS-----L 187

Db 137 llheirkrdslelsqlenklnvttemlkmnatryrelekvysitdlvnnqsvmitll 196

QY 188 DGKCKCPSEQIQSRP-----VQHL----- 208

Db 197 eeqclrifsgdthvspplvqvpphpnsgqytpgllgngneiqrdpgyprdlmppedla 256

QY 209 -----IYKDCSDYYAIGKRSSSEYRVTTPPKNSSFEVYCDMETMGG 249

Db 257 tsptksfpkippvtfinepfkdcqakeaghsvglmkipensngpmqlwcensldpg 316

QY 250 GWTVLQARLDGSTNFTWQDYKAGFNLREFWLGNDXIHLLTKSEKEMILRIDLEDENG 309

Db 317 gwtvlgkrtgdsgvnfrwnykgfgnidgelywlglenlymnsqndnykllieledwsd 376

QY 310 VELYALYDOFYVANEFLKYLRLHVGNYNGTAGDALRFRNKHYNHDLKFFTPDKNDRYPSG 369

Db 377 kkvyaeysfrlepeseefyrlrlgtvggnagdsmmw-----hngkqftldrdkdm- 430

QY 370 NCGLYSSGWFFDACLSANLNGKYH-QKRGV-RNGIFWGTWPGVSEAHPGGYKSSFKE 427

Db 431 ncahfkggwwynacahsnlmgvyrghyrskhgdfwaeyrg-----gsy--slra 482

QY 428 AKMMIRP 434

Db 483 vqmmikp 489

RESULT 15

Y69483

ID Y69483 standard; Protein; 491 AA.

XX Y69483;

XX Y69483;

DT 03-JUL-2000 (first entry)

XX Amino acid sequence of a human angiopoietin (HANG) polypeptide.

XX Human; angiopoietin; HANG; Incyte Clone 2365223; cardiovascular disorder;

cell proliferative disorder; autoimmune disorder; inflammatory disorder;
reproductive disorder.

Homo sapiens.

Key	Location/Qualifiers
Peptide	1..21
Modified-site	/note= "signal peptide"
Modified-site	75
Modified-site	/note= "potential casein kinase II or protein kinase C phosphorylation site"
Modified-site	81
Modified-site	/note= "potential casein kinase II phosphorylation site"
Modified-site	123
Modified-site	/note= "cAMP and cGMP-dependent protein kinase phosphorylation site"
Modified-site	152
Modified-site	/note= "potential casein kinase II phosphorylation site"
Modified-site	160
Modified-site	/note= "potential glycosylation site"
Modified-site	179
Modified-site	/note= "potential tyrosine kinase phosphorylation site"
Modified-site	181
Modified-site	/note= "potential casein kinase II phosphorylation site"
Modified-site	188
Modified-site	/note= "potential glycosylation site"
Modified-site	194
Modified-site	/note= "potential casein kinase II phosphorylation site"
Modified-site	205
Modified-site	/note= "potential casein kinase II phosphorylation site"
Modified-site	360
Modified-site	/note= "potential casein kinase II phosphorylation site"
Modified-site	375
Modified-site	/note= "potential protein kinase C phosphorylation site"
Modified-site	385
Modified-site	/note= "potential protein kinase C phosphorylation site"
Modified-site	395
Modified-site	/note= "potential tyrosine kinase phosphorylation site"
Modified-site	419
Modified-site	/note= "potential casein kinase II phosphorylation site"
Domain	440..452
Modified-site	/note= "potential fibrinogen beta and gamma chains C-terminal domain signature"
Modified-site	479
Modified-site	/note= "potential protein kinase C phosphorylation site"

WO200011164-A1.

02-MAR-2000.

13-AUG-1999; 99WO-US18019.

20-AUG-1998; 98US-0137273.

(INCY-) INCYTE PHARM INC.

Hillman JL, Gorgone GA, Guegler KJ, Corley NC, Patterson C;

WPI; 2000-237647/20.

N-PSDB; 299576.

New polypeptide useful for diagnosing, treating or preventing cardiovascular, cell proliferation, autoimmune/inflammatory, and reproductive disorders comprises amino acid sequence encoding human angiotensin

Claim 1; Fig 1A-F; 73pp; English.

The present sequence represents a human angiotensin (HANG) polypeptide. Nucleic acids encoding HANG were first identified in Incyte Clone 2365223 from an adrenal tissue cDNA library. The HANG polypeptide, and HANG antagonists are useful for treating or preventing a disorder associated with decreased or increased HANG expression or activity,

CC e.g. cardiovascular disorders, cell proliferative disorders, autoimmune
CC and inflammatory disorders, and reproductive disorders. HANG antibodies
CC and polynucleotides are useful for diagnosis of diseases associated
CC with expression of HANG.

XX Sequence 491 AA;

Query Match 21.2%; Score 505; DB 21; Length 491;
Best Local Similarity 26.9%; Pred. No. 4.4e-37;
Matches 131; Conservative 81; Mismatches 137; Indels 138; Gaps 15;

Qy	47	GKCEAGCPYQVSLPITIQLP-----KQFSRIEVEF--KEYQNLKEIVNSLKSCQ	97
Db	42	gk-eeakkcayflvpegritgpcvntkqdasikdmtrmdienlkdvlsrkrkaid	100
Qy	98	DKLQADNGPGRNLLLPSTGAPGEVDNRVRESEVNSKLSKNAKEINVLHGR	157
Db	101	vlqlvvdvgn-----ivnevkllrkesrnmnsrvvtqlymq	136
Qy	158	L-----EKLNLVNMNIENVV-----DSKANLTFVNS-----L	187
Db	137	llheirkrdslelsqienklnvttemlkmatriylevkyasltldvnnqsvmitll	196
Qy	188	DGKSKCPSQEQIOSRP-----VOHL-----	208
Db	197	eeqlrfrsrdthvspplvqvvpqhpnssqytpglllgneiqrdpypdrmlpppda	256
Qy	209	-----IYKDCSDYYAIGKRSEYRVTPDPKNSSEFVYCDMETMGG	249
Db	257	tsptkspfkippvtfinegpfkdcqakeaghsvsygiymikpensngpmqlwcensldpg	316
Qy	250	GWTVLQARLDGSTNTRTWDYKAGFGNLRREFWLGNDKIHLLTKSKEMILRIDLEFNG	309
Db	317	gwtvlgkrtddgsnffrnwenykkfgnldgeywigleniylmsnqdnhykllielewdsd	376
Qy	310	VELVALYDQEVVANEFLKYRLHVGNYNCTAGDALRFNKHYNHDLKFFTPDKNDNRYPSG	369
Db	377	kkvyaeyssfrlepeseefyrlrigtyqgnagdsnmw-----hngkqftldrdkdy-ag	430
Qy	370	NCGLYSSGWFDACLSANLNGKYH-QKRYGV-RNGIFWGTWPGVSEAHPPGGYKSSFKE	427
Db	431	ncanfkhggwyyacahsnlnvgvyrgghyrskhqdgifwaeyrg-----gsy--sira	482
Qy	428	AKMMIRP	434
Db	483	vqmmikp	489

Search completed: February 27, 2001, 12:48:38
Job time: 63 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:36 ; Search time 31.84 Seconds
(without alignments)
936.193 Million cell updates/sec

Title: US-09-442-143-2
Perfect score: 2378
Sequence: 1 MKLANWYLSAVLATYGF.....GYKSSFKKAKMIRPKHKP 439
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2378	100.0	439	2 I37391	fibrinogen-like pr
2	1853.5	77.9	432	2 A27447	cytotoxic T-lympho
3	1849.5	77.8	432	2 I36934	fibrinogen-like pr
4	511.5	21.5	463	2 A38463	fibrinogen beta ch
5	506.5	21.3	312	2 JN0596	fibrinogen-related
6	484.5	20.4	453	1 FGHUGB	fibrinogen gamma-B
7	480.5	20.2	437	1 FGHUG	fibrinogen gamma-A
8	479.5	20.2	479	2 A25052	fibrinogen beta ch
9	470	19.8	468	1 FGBOB	fibrinogen beta ch
10	462	19.4	444	2 S05313	fibrinogen gamma-B
11	461	19.4	491	1 FGHUB	fibrinogen beta ch
12	456	19.2	438	2 A32670	fibrinogen gamma c
13	452	19.0	334	2 J05980	ficolin-A precursor
14	451	19.0	866	2 D44234	fibrinogen alpha c
15	446	18.8	282	2 A35084	fibrinogen-related
16	434.5	18.3	326	2 B47172	ficolin-beta - pig
17	431	18.1	328	2 A05299	fibrinogen beta ch
18	428.5	18.0	323	2 A47172	transforming growt
19	428.5	18.0	432	1 FGLMGS	fibrinogen gamma c
20	423	17.8	326	2 S61517	ficolin-1 precursor
21	423	17.8	1353	1 JH0675	restrictin precurs
22	417.5	17.6	1356	2 A45445	janusin precursor
23	404	17.0	437	1 FGRTGA	fibrinogen gamma-A
24	404	17.0	445	1 FGRTGB	fibrinogen gamma-B
25	403.5	17.0	220	2 S28170	tenascin homology
26	403.5	17.0	417	2 S65944	tenascin-X - pig (
27	401.5	16.9	4135	2 T42629	tenascin-X - bovin
28	397.5	16.7	3566	1 A40701	tenascin-X precurs
29	396	16.7	2019	1 J01322	tenascin precursor

30 393.5 16.5 860 2 I48839 tenascin-X - mouse
31 393.5 16.5 4006 2 T09070 probable tenascin
32 388 16.3 2201 2 A32160 tenascin-C - human
33 386.5 16.3 1746 1 S19694 tenascin precursor
34 386 16.2 1810 1 A32230 tenascin precursor
35 382.5 16.1 1914 2 T42635 tenascin Y precurs
36 356.5 15.0 641 1 A41932 fibrinogen alpha-I
37 346.5 14.6 774 2 A39832 scabrous locus (sc
38 346.5 14.6 774 2 S58998 scabrous protein p
39 215.5 9.1 463 2 T15876 hypothetical prote
40 198 8.3 915 2 T21773 hypothetical prote
41 198 8.3 927 2 T21772 hypothetical prote
42 184.5 7.8 127 2 PC2036 microfibril-associ
43 160 6.7 146 2 T32255 hypothetical prote
44 160 6.7 431 2 T29850 hypothetical prote
45 160 6.7 452 2 T26827 hypothetical prote

ALIGNMENTS

RESULT 1

I37391

fibrinogen-like protein expressed in T lymphocytes (pt49) - human

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: I37391; S47273

R:Ruegg, C.; Pytel, R.

Gene 160, 257-262, 1995

A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib

A:Reference number: I37391; MUID:95369700

A:Accession: I37391

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-439 <RES>

A:Cross-references: EMBL:Z36531; NID:g535184; PIDN:CAA85298.1; PID:g535185

A:Note: submitted to the EMBL Data Library, August 1994

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 100.0%; Score 2378; DB 2; Length 439;
Best Local Similarity 100.0%; Pred. No. 2.8e-157;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLANWYLSAVLATYGFVANNETEIKDERAKDVCPVRLSRGKCEGAGECPYQVS 60

Db 1 MKLANWYLSAVLATYGFVANNETEIKDERAKDVCPVRLSRGKCEGAGECPYQVS 60

Qy 61 LPPLTIOLPKQFSRIEEVFKEVQNLKEIVNSLSKSCQDKLQADDNGDPGRNLLPSTG 120

Db 61 LPPLTIOLPKQFSRIEEVFKEVQNLKEIVNSLSKSCQDKLQADDNGDPGRNLLPSTG 120

Qy 121 APGVGDNRRVRESEYVKNLSSELKNAKEEINVLHGRLEKLNVMNNIENVDSKVANL 180

Db 121 APGVGDNRRVRESEYVKNLSSELKNAKEEINVLHGRLEKLNVMNNIENVDSKVANL 180

Qy 181 TFVYNSLDGKCSKCPSEQIQSRPVQHLIYKDCSDIYAIGKRSETYRVTPDPKNSSEFV 240

Db 181 TFVYNSLDGKCSKCPSEQIQSRPVQHLIYKDCSDIYAIGKRSETYRVTPDPKNSSEFV 240

Qy 241 YCDMETGGGWTVLQARLDGSTNFTRTWDQYKAGFNLRRFWLGNDKIHLLTYSKEMIL 300

Db 241 YCDMETGGGWTVLQARLDGSTNFTRTWDQYKAGFNLRRFWLGNDKIHLLTYSKEMIL 300

Qy 301 RIDLEDFNGVELYALYDQFYVANEFKLYRLHVGNYNGTAGDALRFNKHYNHDLKFFTPD 360

Db 301 RIDLEDFNGVELYALYDQFYVANEFKLYRLHVGNYNGTAGDALRFNKHYNHDLKFFTPD 360

Qy 361 KNDRYPSGNCGLYYSSGWFDACLSANLNGKYYHQYRGVNRGIFWGTWPGVSEAHPGG 420

Db 361 KNDRYPSGNCGLYYSSGWFDACLSANLNGKYYHQYRGVNRGIFWGTWPGVSEAHPGG 420

QY 421 YKSFKEAKMMIRPKHKP 439
Db 421 YKSFKEAKMMIRPKHKP 439

RESULT 2 A27447

cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Saito, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:87175527
A:Accession: A27447

A:Molecule type: mRNA
A:Residues: 1-432 <KQY>

A:Cross-references: GB:M16238; NID:g193304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 77.98; Score 1853.5; DB 2; Length 432;
Best Local Similarity 77.78; Pred. No. 5.6e-121;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

QY 1 MRLPGWLSSAVLATYGLVYANNTEIEIKDERAKDVCVRLESRGKCEEAGECPYQVS 60
Db 1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDAQAACPARLESRGRC-EGSQCPFQLT 58
QY 61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQCKLQADDDGPRNGLLLPSTG 120
Db 59 LPPLTIQLPRQLGSMEEVLKEAVTDLKAVDSLKSCQCKLQADDDHDPGGNG---GNG 114
QY 121 APGEVGDNRVRELSSEVKNLSSELKNAKEEINVLHGRLEKLVNMMNIENYVDSKVANL 180
Db 115 AE-TAEDSRVQELSESQVKNLSSELKNAKDQIQGLQGRLETLHLVNMNIENYVDNKNV 173
QY 181 TFVNSLDGKCKSPQSQEQIQSRPVQHLIYKDCSDYIAGKRSEYRYVTPDPKNSFEV 240
Db 174 TVVNSLDGKCKSPQSQEHMQSQPVQHLIYKDCSDHYVLRSSGAYRYVTPDHRNSSFEV 233
QY 241 YCDMETMGSGTTLQARLDGSTNFTRTWDYKAGFNLRRFELWLNKDKIHLLTKSKEMIL 300
Db 234 YCDMETMGSGTTLQARLDGSTNFTREWKDYKAGFNLRRFELWLNKDKIHLLTKSKEMIL 293
QY 301 RIDLEDFNGVELYALYDQFYVANEFLKYLHVGNTAGDALRNLKHNHDLKFFTTTPD 360
Db 294 RIDLEDFNGLTLYALYDQFYVANEFLKYLHIGNTAGDALRFSRHYNHDLRFFTTTPD 353
QY 361 KDNDRYPSCNGLYSSGWMFDCLSANLNGKYHOKYGRVNGIFWGTWPGVSEAHPGG 420
Db 354 RDNDRYPSCNGLYSSGWMFDCLSANLNGKYHOKYGRVNGIFWGTWPGVSEAHPGG 413
QY 421 YKSFKEAKMMIRPKHKP 439
Db 414 YKSFKEAKMMIRPKHKP 432

RESULT 3 I56934

fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934
R:Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induced
A:Reference number: I56934; MUID:95333285
A:Accession: I56934
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-432 <RES>
A:Cross-references: GB:S7B773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C:Genetics:
A:Gene: musfiblp
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 77.88; Score 1849.5; DB 2; Length 432;
Best Local Similarity 77.48; Pred. No. 1.1e-120;
Matches 340; Conservative 42; Mismatches 50; Indels 7; Gaps 4;

QY 1 MRLANWYLSAVLATYGLVYANNTEIEIKDERAKDVCVRLESRGKCEEAGECPYQVS 60
Db 1 MRLPGWLSSAVLAACR-AVEEHNLTGLEDAQAACPARLESRGRC-EGSQCPFQLT 58
QY 61 LPPLTIQLPKQFSRIEEVFKEVQNLKEIVNSLKKSCQCKLQADDDGPRNGLLLPSTG 120
Db 59 LPPLTIQLPRQLGSMEEVLKEAVTDLKAVDSLKSCQCKLQADDDHDPGGNG---GNG 114
QY 121 APGEVGDNRVRELSSEVKNLSSELKNAKEEINVLHGRLEKLVNMMNIENYVDSKVANL 180
Db 115 AE-TAEDSRVQELSESQVKNLSSELKNAKDQIQGLQGRLETLHLVNMNIENYVDNKNV 173
QY 181 TFVNSLDGKCKSPQSQEQIQSRPVQHLIYKDCSDYIAGKRSEYRYVTPDPKNSFEV 240
Db 174 TVVNSLDGKCKSPQSQEHMQSQPVQHLIYKDCSDHYVLRSSGAYRYVTPDHRNSSFEV 233
QY 241 YCDMETMGSGTTLQARLDGSTNFTRTWDYKAGFNLRRFELWLNKDKIHLLTKSKEMIL 300
Db 234 YCDMETMGSGTTLQARLDGSTNFTREWKDYKAGFNLRRFELWLNKDKIHLLTKSKEMIL 293
QY 301 RIDLEDFNGVELYALYDQFYVANEFLKYLHVGNTAGDALRNLKHNHDLKFFTTTPD 360
Db 294 RIDLEDFNGLTLYALYDQFYVANEFLKYLHIGNTAGDALRFSRHYNHDLRFFTTTPD 353
QY 361 KDNDRYPSCNGLYSSGWMFDCLSANLNGKYHOKYGRVNGIFWGTWPGVSEAHPGG 420
Db 354 RDNDRYPSCNGLYSSGWMFDCLSANLNGKYHOKYGRVNGIFWGTWPGVSEAHPGG 413
QY 421 YKSFKEAKMMIRPKHKP 439
Db 414 YKSFKEAKMMIRPKHKP 432

RESULT 4 A38463

fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
C:Accession: A38463
R>Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745
A:Accession: A38463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEI>
A:Cross-references: GB:M58514; NID:g211779; PIDN:AAA48770.1; PID:g211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 21.58; Score 511.5; DB 2; Length 463;
Best Local Similarity 30.48; Pred. No. 5.2e-28;
Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps 16;

QY 31 KDBRAKDVCPVRLESRGKCEEAGECPYQVSPLPLTIQLPKQFSRIEEVFKEVQV 84
Db 51 QDKQAMKGPITYPDPAGGCKHPLDELGLVLCPTGCE---LQTTLLKQEKTKVPLRLDKLR 107


```
QY 85 -----LKEIVNSLKSCQCKLQADDNGDGRNGLLPSGAPGEVGDNRVRELE 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 VAKFSDSTTMYQVYVNMIDNKLVRKTQKQKD-----NDIILSEYNTMELHYNVIK--D 159
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 135 SEVKNLSSELKNAKEEINVLHGRLEKLNLMNNNIENYVDSKVANLTFVNSLDGCKSKC 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 NLDNNIPSSLRLVRAVDSLHKTKOKL-----ENAIATQT-----DYCRSPC 201
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 195 PSQIQISRPVQHLIYKDCSDYYAIGKRSSEYIRVTPDPKNSFFVYCDMTGGGWTVL 254
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 -----VASCNIPVVSGRECEDYIRKGETSEMYIIQDPFTTPPYVYCDMETDNGGWTLI 256
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 255 QARLDGSTNFTRTWQDYKAGGNLRR-----EFWLGNDKIHLLTKSKEMILRID 303
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 QNRQDGSVNFGRADWEKRGFGNIAKSGGKKYCDTPGGEYWLGNDRKISQLTGKPTKVILIE 316
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 304 LEDFNGVELYALYDQFYVANEFLYRLHVGNYNGTAGDALR--FNKHYN-----HDLK 354
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 317 MEDWNGDKVSALYGGFTIHNEGNYQLSVSNYKGNAGNALMEGASQLYGENRTMTIHNGM 376
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 FETPTDNDRIY----PSGNGCLYSSGGWFDACLSANLNGKYY-----HOKYRGVGN 403
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 377 YFSTYDRDNGWLTTPDRKQCSKEDGGGWYINRCHAANPNRGYWGTYSDMAKHGTTDD 436
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 404 GIFWGTWPGVSEAHPPGGYKSSFKKAKMIRP 434
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 437 GIVVMNKG-----SWY--SMKKMSMKIKP 459
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
JN0596
fibrinogen-related protein HFREP-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
F:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related ge
A:Reference number: JN0596; MUID:93290661
A:Accession: JN0596
A:Molecule type: mRNA
A:Residues: 1-312 <YAM>
A:Cross-references: GB:D14446; NID:g393314; PIDN:BAA03336.1; PID:g393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HFREP-1 #status predicted <MAP>
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 21.3%; Score 506.5; DB 2; Length 312;
Best Local Similarity 36.8%; Pred. No. 6.8e-28;
Matches 118; Conservative 38; Mismatches 108; Indels 57; Gaps 9;

QY 129 RVRESEVKNLSSELKNAKEEINVLHGRLEKLNLMNNNIENYVDSKVANLTFVNSLD 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 QVRLLETRVQKQVKIKQLLQE-----NEVQFLDKGDEDTYVD----- 73
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 189 GKCKSPQSQIQISRPVQHLIYKDCSDYYAIGKRSSEYIRVTPDPKNSFFVYCDMTG 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 -----LGSKRQ-----YADCEIFNDGKLSGFYKIKPLOSAPAEFSVYCDMSD-G 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 249 GGTVTIQLARDLQDSTNFTRTWQDYKAGFNL---RREFWLGNDKIHLLTKSKEMILRIDLE 305
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 GGWTVIQRSDGSSENFNRGNKDYENGFGNFVQKHGEYWLGNLHFLTQEDYTLKIDLA 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 306 DFNGLVELYALYDQFYVANEFLYRLHVGNYNGTAGDALRFNKH-----YHNDLKEFFTT 359
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 DFEKNSRYAQKYNFVGDEKNFELNLTGEYSGTAGDSLGNFHPFVQWASHQRMKFSTW 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 360 DKDNDRYPSCNGLYSSGGWFDACLSANLNGKYYHOKYRG--VRNIGFWGTWPGVSEAH 418
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 238 DRDHDNY--EGNCAEEDSGGWNFNCHSANLNGVYSGPYTAKTDNGIIVWYTW----- 288
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

QY 419 GGYKSSFKKAKMIRPKHFKP 439

I: | | | | | | | | | |

Db 289 HGWWSLSKSVVMKIRPNDFIP 309

RESULT 6

FGHUGB

N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain

C:Species: Homo sapiens (man)

C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 22-Jun-1999

C:Accession: A90494; A90448; A90453; A928203; B28203; I37390; A03126

R:Rixon, M.W.; Chung, D.W.; Davie, E.W.

Biochemistry 24, 2077-2086, 1985

A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.

A:Reference number: A90494; MUID:85252774

A:Accession: A90494

A:Molecule type: DNA

A:Residues: 1-113,'I',115-453 <RIX>

A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:g182438; PIDN:AAB

R:Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.

J. Biol. Chem. 259, 12826-12830, 1984

A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t

A:Reference number: A92448; MUID:85030379

A:Accession: A92448

A:Molecule type: DNA

A:Residues: 286-453 <FOR>

R:Wolfenstein-Todel, C.; Mosesson, M.W.

Biochemistry 20, 6146-6149, 1981

A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain varia

A:Reference number: A90453; MUID:82068993

A:Accession: A90453

A:Molecule type: protein

A:Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <WOL>

R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.

Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988

A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-cha

A:Reference number: A94194; MUID:88217900

A:Accession: A28203

A:Molecule type: protein

A:Residues: 433-449 <FRA>

A:Accession: B28203

A:Molecule type: protein

A:Residues: 433-453 <FR2>

R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.

DNA Seq. 1, 419-422, 1991

A:Title: Polymorphism of the human gamma chain fibrinogen gene.

A:Reference number: I37390; MUID:92119334

A:Accession: I37390

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 75-286 <RES>

A:Cross-references: EMBL:X51473; NID:g31410; PIDN:CAA35837.1; PID:g930064

C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate

ntron, which makes this chain different from the gamma-B chain at positions 434-437 a

C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in p

C:Genetics:

A:Gene: GDB:FGG

A:Cross-references: GDB:119132; OMIM:134850

A:Map position: 4q28-q28

A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1

C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR

ins are contained in the core. Two three-chain coiled coils emerge from this core and

from the distal domain nodes.

C:Function:

A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in

A:Pathway: blood coagulation

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote

F:1-46/Domain: signal sequence #status predicted <SIG>

F:27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>

F:176-415/Domain: fibrinogen beta/gamma homology <FBG>

F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of an
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted
F:49/Disulfide bonds: interchain (to alpha-64) #status predicted
F:78/Binding site: carboxylate (Asn) (covalent) #status predicted
F:161/Disulfide bonds: interchain (to beta-227) #status predicted
F:165/Disulfide bonds: interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to gamma-432-Lys) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to gamma-424-Gln) #status predicted

Query Match 20.4%; Score 484.5; DB 1; Length 453;
Best Local Similarity 29.7%; Pred. No. 3.8e-26;
Matches 141; Conservative 56; Mismatches 178; Indels 99; Gaps 18;

Qy 8 WLSSAVLATYGLVANNTEIEIKDERAKDVCVRLESRGKCEAGCPQVNSLPPLTIQ 67
Db 19 FLSSCTCA-----YVATRDNCCILDERFGSYCPT-----TCGIADFLSTYQTK 61
Qy 68 LPKQFSRIEEVEKQNLKEIYNSLKKSCQCKLQADDDGPGRNGLLLPSTGAPGEVD 127
Db 62 VDKDLQSLIEDILHVENKTSSEVKQLIKAIQ-LTYNPDESCKPMI-----DAAT 109
Qy 128 NRVRELESEVNKLSSELNAKEEINVLHGRLEKLNIVNNNNIENYVDSKVANLTFVNSL 187
Db 110 LKSRKMLEIMKYEASILTHDSIRYLQ-----EIYNSNN-----QKIVNLKQVAQL 157
Qy 198 DGKCKSPQEOIQSPVQHLIYKDCSYIATGKRSEYRYVTPDPKNSFEVYCDMETM 247
Db 158 EAQCOE-PCKDTVQ---IHDTGKDCQDANKGAKOSGLYFIKPLKANOQFLVYCEIDGS 213
Qy 248 GGGWTVQARLDGSTNFTTWDYKAGFNL---RREFWLGNDKIHLLTKSEM--ILR 301
Db 214 GNGWTVQKRLDGSVDFKKNWIOYKGGFGLHSPTGTGTFWLGNEKIHLLTSQSAIPYALR 273
Qy 302 IDLEDNGVELYALYDQFVYANEFKYRLHVGNY-NGTAGDAL-RFNKYNHDLKFFT-- 357
Db 274 VELEDNGRTSTADYAMFKVGPADKRYLYAYFAGDGADGDFDGDPSDKFFTSH 333
Qy 358 -----TPDKNDRYPGNCGLYYSGWFWFACLSANLNGKYH-----QYRGVNRG 404
Db 334 NGMQFSTWMDNDKF-EGNCAEODGSGWWMKCHAGLNGVYQGGYTSKASTPNGVDNG 392
Qy 405 IFWGTWP-----GVSEA---HPGGYKSSFEAKMMIRPKH 436
Db 393 IIWATKTRWYSMKKTKMIIPNRLTIGEGQOHLGGAK-----QVRPEH 438

RESULT 7
FGHUG
fibrinogen gamma-A chain precursor - human
N:Alternate names: coagulation factor I
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 25-Feb-1985 #text change 21-Jul-2000
C:Accession: A90470; B90494; C94433; B93956; B92448; I37393; A40698; H54223; A03125; C37
R:Chung, D.W.; Chan, W.Y.; Davie, E.W.
Biochemistry 22, 3250-3256, 1983
A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma
A:Reference number: A90470; MUID:83283434
A:Accession: A90470
A:Molecule type: mRNA
A:Residues: 1-437 <CHU>
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: B90494
A:Molecule type: DNA
A:Residues: 1-113, 'I', 115-437 <RIX>
A:Cross-references: GB:X02415; GB:M10014; NID:gl82436; PIDN:AAB59531.1; PID:gl82439

R:Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in: Protides of the Biological Fluids, Proc. 28th Colloq., Peters, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
A:Reference number: A94433
A:Accession: C94433
A:Molecule type: protein
A:Residues: 27-437 <HEN>
R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A:Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains:
A:Reference number: A93956; MUID:83247396
A:Accession: B93956
A:Molecule type: mRNA
A:Residues: 276-437 <KAN>
R:Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near t
A:Reference number: A92448; MUID:85030379
A:Accession: B92448
A:Molecule type: DNA
A:Residues: 286-437 <FOR>
R:Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A:Title: Isolation and characterisation of cDNA clones for the alpha- and gamma-chai
A:Reference number: I37393; MUID:84069777
A:Accession: I37393
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 209-270 <RES>
A:Cross-references: EMBL:X00086; NID:g31445; PTDN:CAA24944.1; PID:g577055
R:Bernagnoli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with
A:Reference number: A40698; MUID:93286185
A:Accession: A40698
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <BER>
A:Experimental source: thrombin-activated platelets
A:Note: sequence extracted from NCBI backbone (NCBIP:133734)
R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lip
A:Reference number: A54223; MUID:94162201
A:Accession: H54223
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <KUN>
A:Note: identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Contents: annotation; review, disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.
in: Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., F
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Contents: annotation; disulfide bonds
R:Blomback, B.; Hessel, B.; Hoggy, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080
A:Contents: annotation; disulfide bonds
R:Hoepflich, P.D.; Doolittle, R.F.
Biochemistry 22, 2049-2055, 1983
A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bond
A:Reference number: A90467; MUID:83231465
A:Contents: annotation; quaternary structure, disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Horwitz, B.H.; Varadi, A.; Scheraga, H.A.

```
Db      62 VDKDLQSLIEDILHOVENKNTSEVKOLIKAI0-LYNPDDESKPNNI-----DAAT 109
QY     128 NRRELESEVNKLSELNKAKEETINVHGRLEKLNVLNMNIENIVDSKVANLTFVNSL 187
       : ::::: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db    110 LKSRLMEELTKYEASILTHTDSSIRYLQ-----EIYNSNN-----QKIVNLKEVAQL 157
       : :::~: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY     188 DGKSCKPSPSQEQISRPVOHLIIKYDCSDYYAIGKRSETRYRTPDPKNSSFVEYCDMETM 247
       : :::~: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db    158 EAQCQE-PCKDVTQ---IHDTCKDCQDIANKAKQSGLYFIKPLKANQQFLVYCEIDGS 213
       : :::~: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY     248 GGGTWTVALRDGSTNRPTRWQDYKAGFGML----RRFWLGNDKIHLTITKKEM--ILR 301
       |||| ~|||| |:| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db    214 GNGWTVFKRLDGSVDFPKWNIOIQEGFCHLSPTGTTEFFWLGNKEIHLISTQSAIPYALR 273
       : :::~: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY     302 IDLEDENGVELYALYDOFYANEELKXRVLRHVNY-NCTAGDAL-RNKHYNHDLRKFFT-- 357
       ::::::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db    274 VELEDNWGRTSTADYAMFKVGPRADKYRIITYAFAGGDAGADFDDGFDPSPDKFFTS 333
       : :::~: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY     358 -----TPDKDNDRYPGNCGLLYSGCWFFDACLSANLCNKYYH-----QKYRGVRNG 404
       ||||: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db    334 NGHQFSFTWDNDNKF-EGNCAEODGSGGWNNWKCHAGHLNGVVYQGTYYSKASTPNGVDNG 392
       : :::~: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
QY     405 IFWGTTW 410
        I I II
Db    393 IIAWTW 398

RESULT      8
A25052
N;Contains: fibrinopeptide B
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
C;Accession: A25052; A03124; B03124
R;Bohonus, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A;Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A;Reference number: A25052; MID:87076582
A;Accession: A25052
A;Molecule type: mRNA
A;Residues: 39-479 <BO>
A;Cross-references: GB:M14773; NID:g2l3191; PIDN:AAR49261.1; PID:g2l3192
R;Cottrell, B.A.; Doolittle, R.F.
Biochim. Biophys. Acta 453, 426-438, 1976
A;Title: Amino acid sequences of lamprey fibriнопепptides A and B and charac
A;Reference number: A03120; MID:77065679
A;Accession: A03124
A;Molecule type: protein
A;Residues: 1-36 <COtl>
A;Accession: B03124
A;Molecule type: protein
A;Residues: 37-42 <COR>>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibr
C;Keywords: blood coagulation; glycoprotein; sulfoprotein
F;1-36/Product: fibrinopeptide B #status experimental <FPB>
F;37-479/Product: fibrin beta chain #status experimental <MAT>
F;90-219/Domain: fibrinogen disulfide ring homology <FDB>
F;229-477/Domain: fibrinogen beta/gamma homology <FBG>
F;17/Binding site: sulfate (Tyr) (covalent) #status experimental
F;23/Binding site: carbohydrate (Asn)(covalent) #status experimental
```

Query Match	20.2%;	Score 480.5;	DB 1;	Length 437;
Best Local Similarity	31.2%;	Pred. No. 6.8e-26;		
Matches 133;	Conservative 53;	Mismatches 171;	Indels 69;	Gaps 15;

QY	8	WLSGAVLATYGLVNVANNETEIEIKDRAKDVCVRLESRGKCEAGECPCYQVSLPPLTIQ	67
Db	19	FLSSTCVA-----YVATRDNCCLIDRFSGSYCT-----TCGIADELSTYQTK	61

QY	68	LPKQFSRTEEFKEVQNLUKEIVNSLKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGD	127

```
F;215-464/Domains: fibrinogen beta/gamma homology <FBG>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F;21-22/Cleavage site: Arg-Gly (thrombin) #status experimental  
F;371/Binding site: carbonylhydride (Asn) (covalent) #status predicted  
F;372-373/Cleavage site: Arg-Thr (plasmin) #status experimental
```

	Query Match 19.8% ; Score 470; DB 1; Length 468;
	Best Local Similarity 30.6%; Pred. No. 4e-25;
Matches 129; Conservative 57; Mismatches 149; Indels 86; Gaps 13;	

QY	61	LPPPTIQLPKQSRIEE-VPEKVNLEKEIVNSLKKSCDQC--KLQADDNGDPGRNGLLLP	117
	: :	: :: :::	:
DB	82	LCPTGCCKLDQTFLVROEPIRKISIEDLRNTVDVSRTSSSTFYITLLKNMKGR-----	135
	: :	: :: :::	:
QY	118	STGAPGEVGDNVRVESEYNKLSSELNAKEEVNLHGLEKLNLYNMNNNIENVDSKV	177
	: :	: :: :::	:
DB	136	-----NQGVODNEVVNEYSS-----HLEKHQLYIDETVKNNIPTKL	172
	: :	: :: :::	:
QY	178	ANLTFFVYNSLDGKCSPQBQIQSR-----PVQHLYIKDCSDYYAIGKRSES	225
	: :	: :: :::	:
DB	173	RVLRSILENLSRKIQLKLESVDYSTOMEYCRLTPCTVTCLNPV--VSGECEKIIRNETGETS	230
	: :	: :: :::	:
QY	226	TYRVTPDKNSFEVCMDMETMGCGWTVALQRDLGSTNFTRTWODYKAGGNLRR-----	280
	: :	: :: :::	:
DB	231	MYLIQPEDSSXPYVYCDMKTCKGGWTVIONRQDGSLDFGRKWPDYPQGFGFNIAEGK	290
	: :	: :: :::	:
QY	281	-----EFWLGNDAHLTKSKEMILRIDLEDENFVELALDYFYVANEFKYRLHVHG	333
	: :	: :: :::	:
DB	291	KYCVGPWEYLWNDRISOLTNMTGPTKLLIEMEDWKGDVKATALYEGFTVQNANKYQLSVS	350
	: :	: :: :::	:
QY	334	NNYGTAGDAL-----RFNKHYN-HDLKFPTFPDDKDNDRY----PSGNCGLYSSGW	380
	: :	: :: :::	:
DB	351	KYKGTAGNALLEGASQLVENRTTFIHNSPFYSYRDNDGKWTTDPKQCSKEDGGWW	410
	: :	: :: :::	:
QY	381	FDACLSANLGKYYY-----HQKYRGVRNGIFWGTHPGVSEAHPGGYKSFKFAKMHIR	433
	: :	: :: :::	:
DB	411	YNRCHAAPNPGRYWYGGAITYDMAKHGTDGQVVMNVQQ-----SWY--SMKKMSMKIR	462
	: :	: :: :::	:
QY	434	P 434	
DB	463	P 463	

RESULT 10

S05313

fibrinogen gamma-B chain precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999

C:Accession: S05313

R:Brown, W.M.; Dziegielewski, K.M.; Foreman, R.C.; Saunders, N.R.

Nucleic Acids Res. 17, 6397, 1989

A>Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibrinogen

A:Reference number: S05313; PMID:89366676

A:Accession: S05313

A:Molecule type: mRNA

A:Residues: 1-444 <BRO>

A:CROSS-references: EMBL:X15556; NID:g349; PIDN:CAA33562.l.; PID:g350

A>Note: The authors translated the codon AGT for residue 105 as Ala and ART for residue 106 as Aspartate.

C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-44/Product: fibrinogen gamma-B chain #status predicted <MAT>

F;174-414/Domains: fibrinogen beta/gamma homology <FBG>

	Query Match 19.4% ; Score 462; DB 2; Length 444;
	Best Local Similarity 30.5%; Pred. No. 1.3e-24;
Matches 142; Conservative 51; Mismatches 164; Indels 108; Gaps 19;	

Qy	9	LSSAVLATGYELFWANNTEIEKERADKVCPRVRESKCEAGECPYQVSLPLTLQL	68
		::: ::	:
Db	18	LSLACLA-----YVATRDNCCILDREFGSYCP-----TCGIADFNNYQTSV	60
		::: ::	:

F:31-491/Product: fibrinogen beta chain #status experimental <MAT>
F:31-44/Product: fibrinopeptide B #status experimental <AP>
F:45-491/Product: fibrin beta chain #status experimental <PBG>
F:45-47/Region: polymerization site
F:99-228/Domain: fibrinogen disulfide ring homology <FPG>
F:238-487/Domain: fibrinogen beta/gamma homology <PBG>
F:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:44-45/Cleaveage site: Arg-Gly (thrombin) #status experimental
F:95/Disulfide bonds: interchain (to alpha-55) #status experimental
F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
F:223/Disulfide bonds: interchain (to alpha-184) #status experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
F:231-316,241-270,424-437/Disulfide bonds: #status experimental
F:394/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.4%; Score 461; DB 1; Length 491;
Best Local Similarity 28.7%; Pred. No. 1.8e-24;
Matches 133; Conservative 57; Mismatches 161; Indels 112; Gaps 14;

QY 27 TEEKDERAKDVCVRLESRGKEAGE-----CPQVSLPLTLIQLPKOF-SRIEEVEK 80
DB 81 TOKKVERAPDA-----GGCLHADPDGLVLCPTGCOLEALLOOERPIRNSVDELNN 132
QY 81 EVONLKEIVNS-----LKSCQDCKLQADDNGDPGRNGLLPLSTGAPGEVDNRVREL 133
DB 133 NVEAVSOTSSSFQWYLLKDLWKRQKQVKN-----165
QY 134 ESEYNKLSSELKNAKEEINVLHGRLEKLNVMNNIENYVDSKVANLTFVNSLDGCKSK 193
DB 166 ENVVNEYSSE-----LEKHOLYIDETVNSNIPNLRVLRILENLSRKIOK 211
QY 194 CPSOEOIQ-----SRPVOHLIYKDCDYAIGKRSSSTYRVTDPKNSSEFVYCD 243
DB 212 LESDVSQMEYCRCTCTVSCNIPVVGKKEELIRGGTSETMYLIQDSSVVKPYRVCYD 271
QY 244 METGGGWTVLQARLDGSTNFTRTWQYKAGFCN-----LRREFWLGNDKIHIL 291
DB 272 MNTENGWTVIQNRQDGSVDFGRKWDYKQGFNGVATNTDGRNYCGLPGEYWLGNQDKISO 331
QY 292 LTKSKEMILRIDLDFNGVELYALYDQFVANEFLYRLHVGNYNTAGDALR-----344
DB 332 LTRMGPTELLIMEDWKGDVKAHYGGFTVQNEANKYQISVKNYRGCTAGNALMDGASOLM 391
QY 345 -FNKHYN-HDLKFFTPDKNDRY-----PSGNCGLYSSGWFWFDCLSANLNGKYY-----394
DB 392 GENRTMTIHNGMFFSTYDNDNGWLTSDPRKOCSEKEDGGGWYNRCHAANPNRYTWGGQ 451
QY 395 ---HOKYRGVRNGIFWGTWPGVSEAHPGGYKSSFKKAKMIRP 434
DB 452 YTDWMAKHGCTDGVVMMNWKG-----SWY--SMRKMMSKIRP 486

RESULT 12
A32670
fibrinogen gamma chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A:Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A:Reference number: A32670; MUID: 90241882
A:Accession: A32670
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-438 <PAS>
A:Cross-references: GB:J02894; NID:g214139; PIDN:AAA49709.1; PID:g214140
R:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A:Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
A:Reference number: I51416; MUID: 91146806

A:Accession: I51416
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-58 <BHA>
A:Cross-references: GB:M35548; NID:g214141; PIDN:AAA03247.1; PID:g214142
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation
F:173-413/Domain: fibrinogen beta/gamma homology <PBG>

Query Match 19.2%; Score 456; DB 2; Length 438;
Best Local Similarity 30.4%; Pred. No. 3.4e-24;
Matches 130; Conservative 69; Mismatches 158; Indels 70; Gaps 17;

QY 10 SSAVLATYGLVYVANNETEEIKDERAKDVCVRLESRGKEAGECPYQVSLPLTLIQLP 69
DB 14 SLALLSSAFNGNIIPNTDNCCLDGRFGEYCPT-----TCGIS 50
QY 70 KQFSRIEE-VFKEVQNKEIVNSLKSCQDCKLQADDNGDPGRNGLLPLSTGAPGEVDN 128
DB 51 DFLNRYOENVDTDLQYLENLLTQISNSTSGTTIIVEHLIDSGKKPATSPQTAI-----DP 105
QY 129 RVRELESEYNKLSSELKNAKE-EINVLHGRLEKLNVMNNIENYVDSKVANLTFVNSL 187
DB 106 MTKSKTCWKKL-TDMKNYYOYEENILY--LQEVYSSNQNKI-FLKOKIANLEL-----156
QY 188 DGKSKCPSQEQIQSRPVOHLIYKDCDYAIGKRSSSTYRVTDPKNSSEFVYCDMETM 247
DB 157 --OCQO-PCRDVTQ---IQEFTGDKQEVANKGARLSGLYIKPLKAKQOFLVYCEIEPS 210
QY 248 GGGWTVLQARLDGSTNFTRTWQYKAGF-----NLRREFWLGNDKIHILTKSKEM--ILR 301
DB 211 GSAWTVIQRDLGDSVNFKNWQYREGFYLSPLNDKTEFWLGNKEKIHLLTQSTIPYVMR 270
QY 302 IDLEDFNGVELYALYDQFVANEFLYRLHVGNY-NTAGDAL-----RFNKHV-NH 351
DB 271 IELEDNSNQSTADYSTFRLGSEKDNRYFTYAYFIGDAGDAFDGDFGDDPSDKFTYSH 330
QY 352 DLKFFFTPDKNDRYPSGNCGLYSSGWFWFDCLSANLNGKYYH-----QKRYGRVN 403
DB 331 NGQWFTFDKNDKF-DGNCAEQDGSQWNRCHAHLNGKYYOGGTYSEADSPSGYDN 389
QY 404 GIFWGTW 410
DB 390 GIWATW 396

RESULT 13
JC5980
ficollin-A precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-May-1998 #sequence_revision 29-May-1998 #text_change 18-Feb-2000
C:Accession: JC5980
R:Fujimori, Y.; Harumiya, S.; Fukumoto, Y.; Miura, Y.; Yagasaki, K.; Tachikawa, H.; F
Biochem. Biophys. Res. Commun. 244, 796-800, 1998
A:Title: Molecular cloning and characterization of mouse ficollin-A.
A:Reference number: JC5980; MUID: 98205801
A:Accession: JC5980
A:Molecule type: mRNA
A:Residues: 1-334 <FUJ>
A:Cross-references: DDBJ:AB007813; NID:g2957011; PIDN:BAA25126.1; PID:d1026054; PID:g
A:Experimental source: liver
C:Comment: This protein consists of both collagen- and fibrinogen- like domains.
C:Superfamily: fibrinogen beta/gamma homology
F:1-21/Domain: signal sequence #status predicted <SIG>
F:50-64,68-106/Domain: collagen-like #status predicted <COL>
F:123-334/Domain: fibrinogen beta/gamma homology <PBG>

Query Match 19.0%; Score 452; DB 2; Length 334;
Best Local Similarity 34.4%; Pred. No. 4.4e-24;
Matches 114; Conservative 35; Mismatches 106; Indels 76; Gaps 12;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2001, 12:47:34 ; Search time 21.07 Seconds
(without alignments)
374.141 Million cell updates/sec

Title: US-09-442-143-2

Perfect score: 2378

Sequence: 1 MRLANWYWLSSAVLATYGL.....GYKSSFKEAKMIRPKHFKP 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2.6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2.6/ptodata/2/iaa/6_COMB.pep.*

4: /cgn2.6/ptodata/2/iaa/PCRUS_COMB.pep.*

5: /cgn2.6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	524	22.0	314	1	US-08-525-505A-2
2	522	22.0	496	1	US-08-373-579-6
3	522	22.0	496	2	US-08-418-595-6
4	522	22.0	496	2	US-08-665-926-6
5	522	22.0	496	3	US-09-162-437-6
6	506.5	21.3	286	3	US-08-960-507-20
7	506	21.3	312	1	US-08-525-505A-4
8	505	21.2	491	2	US-08-933-821-4
9	505	21.2	491	3	US-08-960-507-4
10	489	20.6	346	3	US-08-960-507-19
11	487	20.5	497	1	US-08-373-579-4
12	487	20.5	497	2	US-08-418-595-4
13	487	20.5	497	2	US-08-665-926-4
14	487	20.5	497	2	US-08-348-492-4
15	487	20.5	497	3	US-09-162-437-4
16	481.5	20.2	453	1	US-08-206-176-6
17	480.5	20.2	493	2	US-08-933-821-2
18	480.5	20.2	493	3	US-08-960-507-2
19	480.5	20.2	498	1	US-08-373-579-2
20	480.5	20.2	498	2	US-08-418-595-2
21	480.5	20.2	498	2	US-08-665-926-2
22	480.5	20.2	498	2	US-08-348-492-2
23	480.5	20.2	498	3	US-09-162-437-2
24	468	19.7	411	1	US-08-232-532-1
25	468	19.7	411	2	US-08-748-150-1
26	468	19.7	411	4	PCR-US95-05168-1
27	467.5	19.7	509	2	US-08-665-926-8
28	461	19.4	491	1	US-08-206-176-4
					Sequence 2, Appli
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 20, Appl
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 19, Appl
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 6, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 8, Appli
					Sequence 4, Appli

29 458.5 19.3 454 3 US-08-434-099A-27
30 458.5 19.3 454 3 US-08-434-099A-28
31 446 18.8 282 3 US-08-812-586-49
32 444 18.7 214 3 US-08-960-507-21
33 439.5 18.5 236 3 US-08-886-269-2
34 439.5 18.5 236 3 US-09-167-647-2
35 439.5 18.5 470 2 US-08-933-821-6
36 439.5 18.5 470 2 US-08-960-507-6
37 438.5 18.4 236 3 US-08-886-269-1
38 438.5 18.4 236 3 US-09-167-647-1
39 431.5 18.1 236 3 US-08-886-269-4
40 431.5 18.1 236 3 US-09-167-647-5
41 429.5 18.1 236 3 US-08-886-269-3
42 429.5 18.1 236 3 US-09-167-647-4
43 421 17.7 1358 1 US-08-404-665-4
44 421 17.7 1358 1 US-08-404-671-4
45 421 17.7 1358 1 US-08-404-781-4

ALIGNMENTS

RESULT 1
US-08-525-505A-2
; Sequence 2, Application US/08525505A
; Patent No. 5807711
; GENERAL INFORMATION:
; APPLICANT: HARA, HIROSHI
; APPLICANT: YOSHIMURA, HIROMITSU
; APPLICANT: MATSUKI, YUMIKO
; APPLICANT: SHINDO, SAEKO
; APPLICANT: HANADA, KAZUNORI
; TITLE OF INVENTION: PARENCHYMAL HEPATOCYTE GROWTH SUBSTANCE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525.505A
; FILING DATE: 22-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00455
; FILING DATE: 22-MAR-1994
; APPLICATION NUMBER: JP 05-063905
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-505A-2

RESULT 4
US-08-665-926-6
; Sequence 6, Application US/08665926
; Patent No. 5851797
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/665,926
; APPLICATION NUMBER: US/08/665,926
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert J. Cobert
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-2113
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-595-6

Query Match 22.0%; Score 522; DB 2; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.9e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;

Qy 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 26 MDSIGKKYQVHGSCSYTFLPEMDNCRSSSPYVNAVQDAPLEYDDSVQRLQVLEN 85
Qy 85 LKE-----IVNSLKKSCQCKLQADDNGDPGRNGLLLPSTGAPGEVDN--- 128
Db 86 IMENNTQWLKLENYIQDNMKKEMVEIQONAVQN-----QTAVMIEIGTNLLNQ 134
Qy 129 -----RVRELESEV-----NKLSELKNAKEEINVHLGR---LEKL 161
Db 135 TAEQTRKLTDEVAQVNLQTTRELEQLLEHSLSTNKLKLEQILDQTSSEINKLQDKNSFLEKK 194
Qy 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLOSIKEEKDQQLVLSKQNSIEELEKKIVTATVNSVLQKQOHDLMET 254
Qy 184 VNSLDGKCSKCPSEQIQSRPVQHLIYKDCSDYAIAGKRSSETYRVTDPKNSSEFVEYCD 243
Db 255 VNNLLTMSTNSAKDPTVAKEEQISFRDCAEVKSGHTNGIYTLTPPNSTEIKAYCD 314
Qy 244 METMGCGTTLQARLDGNTFTWQDYKAGFGNLRREFWLGNDKIHLLTKSEKILRID 303
Db 315 MEAGGGGWTIIQRREDGSDVDFTWKYKVGFGNPGSGEYWLGNFVSLTNOQRYVLKIH 374
Qy 304 LEDFNGVELYALDYQFVYANEFKLYRLHVGNYNGTAGDALRNLKHNHDLKFFETTPDKON 363
Db 375 LKDWEGNEAYSLYEHFYLSSEELNRIHLKGLTGTAGKISSISQPGND-----FSTKDGDN 430
Qy 364 DRYPSCNGCLYSSGWWFDACLSANLNGYHYHQYKRGVR-NGIFWGTWPGVSEAHPPGGY 422
Db 431 DKIC-KCSQMLTGGWFDACGPSNLNGMYYPQRTNFKNGIKYIWKG-----SGY- 482
Qy 423 SSFKEAKMWRPKHF 437
Db 483 -SLKATTMMIRPADF 496

Query Match 22.0%; Score 522; DB 2; Length 496;
Best Local Similarity 27.9%; Pred. No. 5.9e-40;
Matches 138; Conservative 74; Mismatches 159; Indels 124; Gaps 15;
Qy 43 LESRGKCE---EAGECPYQVSLPPL-----TIQ--LPKQFSRIEEVFKEVQN 84
Db 26 MDSIGKKYQVHGSCSYTFLPEMDNCRSSSPYVNAVQDAPLEYDDSVQRLQVLEN 85
Qy 85 LKE-----IVNSLKKSCQCKLQADDNGDPGRNGLLLPSTGAPGEVDN--- 128
Db 86 IMENNTQWLKLENYIQDNMKKEMVEIQONAVQN-----QTAVMIEIGTNLLNQ 134
Qy 129 -----RVRELESEV-----NKLSELKNAKEEINVHLGR---LEKL 161
Db 135 TAEQTRKLTDEVAQVNLQTTRELEQLLEHSLSTNKLKLEQILDQTSSEINKLQDKNSFLEKK 194
Qy 162 NLV-----NMNNIENYVDSKVANLTF-----V 183
Db 195 VLAMEDKHIIQLOSIKEEKDQQLVLSKQNSIEELEKKIVTATVNSVLQKQOHDLMET 254
Qy 184 VNSLDGKCSKCPSEQIQSRPVQHLIYKDCSDYAIAGKRSSETYRVTDPKNSSEFVEYCD 243
Db 255 VNNLLTMSTNSAKDPTVAKEEQISFRDCAEVKSGHTNGIYTLTPPNSTEIKAYCD 314
Qy 244 METMGCGTTLQARLDGNTFTWQDYKAGFGNLRREFWLGNDKIHLLTKSEKILRID 303
Db 315 MEAGGGGWTIIQRREDGSDVDFTWKYKVGFGNPGSGEYWLGNFVSLTNOQRYVLKIH 374
Qy 304 LEDFNGVELYALDYQFVYANEFKLYRLHVGNYNGTAGDALRNLKHNHDLKFFETTPDKON 363
Db 375 LKDWEGNEAYSLYEHFYLSSEELNRIHLKGLTGTAGKISSISQPGND-----FSTKDGDN 430


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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-525-505A-4

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Query Match 21.3%; Score 506; DB 1; Length 312;
Best Local Similarity 44.6%; Pred. No. 8.8e-39;
Matches 107; Conservative 25; Mismatches 88; Indels

[illegible]

```

RESULT      8
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER TYPE: 3.5 inch, 1.44 Mb fl
; MEDIUM TYPE: 3.5 inch, 1.44 Mb fl
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-933-821-4

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Query Match 21.2%; Score 505; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 2.2e-38;
Matches 131; Conservative 81; Mismatches 137; Indels 1

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Query Match      21.3%; Score 506.5; DB 3; Length 286;
Best Local Similarity 36.0%; Pred. No. 6.9e-39;
Matches 112; Conservative 49; Mismatches 121; Indels 29; Gaps

128 NRVRELESEVNKLSSELKNAKEEINVLHGRLKLNLVNMMNIENYVDSKVANLTFVNSL 187
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4  DOLQVLVSKQNSITEELEKKIVTAVNNSVLQKQOHDLMETVNNL-----LTMNSTN 56
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

188 DGKSKCPSQIQSRPVQHLYIKDSDYYAIGKRSSSEYRYVPDPKNSSEFYCDMETM 247
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57. SAKOPTVAKEQIS-----FRDCAEVPKSGHTTINGIYTLTFPNSTEIKAxCDMEAG 108
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

248 GGGWTVLQARLDGSTNTRTWQYKAGFGLRRREFWGNDKIHLTLTKSKEMILRIDLEDF 307
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
109 GGGWTTIQRREDGSGFQRTWKKEYKVGFGNPSGEYVLGNFEVSQLTNQOYRYVLKHLKDW 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

308 NGVELYALYDOFYVANEFLKRYLRHGVNNGCTAGDALRFNKHYNHDLKFTTTPDKONDYP 367
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
169 EGNRAYSLYEHFYLSSEELNRYHLKGLTGTAGKISSIOPGND-----FSTKGDGNDKCI 224
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

368 SGNGCLYSSGWWPDACLSANLKGYYHQYRGVR-NGIFWGTWPVCVSEAHPPGGYKSSF 426
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
225 C-KCSQMLTGWWFDCGSPNLNGWYYPQONTNKEGLIKWYWKG-----SGY--SLK 275
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

427 EAKWMIRPKHF 437
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
276 ATTMMIRPADF 286
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

-08-525-505A-4
 Sequence 4, Application US/08525505A
 Patent No. 5807711
 GENERAL INFORMATION:
 APPLICANT: HARA, HIROSHI
 APPLICANT: YOSHIMURA, HIROMITSU
 APPLICANT: MATSUKI, YUMIKO
 APPLICANT: SHINDO, SAEKO
 APPLICANT: HANADA, KAZUNORI
 TITLE OF INVENTION: PARENCHYMAL HEPTOCYTE GROWTH SUBSTANCE
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 STREET: ARLINGTON
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/525,505A
 FILING DATE: 22-SEP-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP94/00455
 FILING DATE: 22-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 05-063905
 FILING DATE: 23-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220

TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994

```

; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,595
FILING DATE: 06-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-418-595-4

Query Match 20.5%; Score 487; DB 2; Length 497;
Best Local Similarity 32.4%; Pred. No. 1e-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;
QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQCKLQADDDGDPGRN 112
DB 145 LTVETQVLNQTSLRIQLLENSLSYKLEKQLLOQTNEILKIHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVKNLSSELKNAKEEINVHLG-----RLEK-L 161
DB 192 SLL-----EHLKLEME---GKHKEELDTLKEEKENLQGLVTRQYIIQLEKQL 237
QY 162 NLVNMNIENYVDSKVANLTFVNSLDGKCSK---CPSQEQIQSRPVQHLIYKDCSDYYA 218
DB 238 NRATTNN--SVLQKQOQLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADVIQ 290
QY 219 IGRKRSSETYRV---TPDPKNSSEFYCDMETGGGWTVLOARLDGSGTNRFTWQDYKAG 274
DB 291 AGFNKSGIYTIYINNMPEPK---KVCNMDVNGGWTVIQHRDGSGLDFQGRKKEYKMG 346
QY 275 FGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYLHVG 334
DB 347 FGNPSGEYWLGNFEFAITSQRYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYK 406
QY 335 YNGTAGDALRKNKYNHDLKFTTTPDKNDRYPSGNCGLYSSGWNFDACLSANLNGKYY 394
DB 407 HTGTAGKQSSLIH-GAD---FSTKADNDNCMC-KCALMLTGGWFDACGPNLNGMFY 461
QY 395 HQ-KYRGVRNGIFWGTWPGVSEAHGPGYKSSFKKAKMMIRPKHF 437
DB 462 TAGQNHGKLGKIKWHYFKGPS-----YSLRSTTMMIRPLDF 497

RESULT 13
US-08-665,926-4
; Sequence 4, Application US/08665926

Patent No. 5851797
GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert J. Cobert
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-926-4

Query Match 20.5%; Score 487; DB 2; Length 497;
Best Local Similarity 32.4%; Pred. No. 1e-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;
QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQCKLQADDDGDPGRN 112
DB 145 LTVETQVLNQTSLRIQLLENSLSYKLEKQLLOQTNEILKIHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRESEVKNLSSELKNAKEEINVHLG-----RLEK-L 161
DB 192 SLL-----EHLKLEME---GKHKEELDTLKEEKENLQGLVTRQYIIQLEKQL 237
QY 162 NLVNMNIENYVDSKVANLTFVNSLDGKCSK---CPSQEQIQSRPVQHLIYKDCSDYYA 218
DB 238 NRATTNN--SVLQKQOQLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADVIQ 290
QY 219 IGRKRSSETYRV---TPDPKNSSEFYCDMETGGGWTVLOARLDGSGTNRFTWQDYKAG 274
DB 291 AGFNKSGIYTIYINNMPEPK---KVCNMDVNGGWTVIQHRDGSGLDFQGRKKEYKMG 346
QY 275 FGNLRREFWLGNDKIHLLTKSKEMILRIDLEDFNGVELYALYDQFYVANEFLKYLHVG 334
DB 347 FGNPSGEYWLGNFEFAITSQRYMLRIELMDWEGNRAYSQYDRFHIGNEKQNYRLYK 406
QY 335 YNGTAGDALRKNKYNHDLKFTTTPDKNDRYPSGNCGLYSSGWNFDACLSANLNGKYY 394
DB 407 HTGTAGKQSSLIH-GAD---FSTKADNDNCMC-KCALMLTGGWFDACGPNLNGMFY 461
QY 395 HQ-KYRGVRNGIFWGTWPGVSEAHGPGYKSSFKKAKMMIRPKHF 437
DB 462 TAGQNHGKLGKIKWHYFKGPS-----YSLRSTTMMIRPLDF 497

RESULT 14
US-08-348-492-4

Sequence 4, Application US/08348492
Patent No. 5879672
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,492
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 330B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 347-7000
TELEFAX: (914) 347-2113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-492-4

Query Match 20.5%; Score 487; DB 2; Length 497;
Best Local Similarity 32.4%; Pred. No. le-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;
QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
Db 145 LTDVETQVNLQTSRLIEQLLENSLSTYKLEKQLQQTNEILKIHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRELESEVKNLSSELKNAKEEINVLHG-----RLEK-L 161
Db 192 SLL-----EKKILEME---GKHREELTLKEKENLQGLVTRQYIYIQLKQL 237
QY 162 NLVNMNNIENYDSKVANTFFVNSLDGKSK---CPSQEQIQSRPVQHLIYKDCSYIA 218
Db 238 NRATTNN--SVLQKQQLLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FRDCADVQ 290
QY 219 IGRSSEYTRV---TPDPKNSFEVYCDMETGGGWTVLQARLDGSTNTRTWQDYKAG 274
Db 291 AGFNKSGIYTIINNPEPK-----KVCNMDVNGGGWTVIQHRDGLDLPQGWKEYKMG 346
QY 275 FGNLREFFWLGNDKIHLTKSKEMILRIDLEDFNGVELYALYDQVYVANEFLYRLHGVN 334
Db 347 FGNPSEYWLGNFEFATISQRYMLRIELMDWEGNRAYSQYDRFHLCGNEKQYRLYK 406
QY 335 YNGTAGDALFRNKHNDLFFFTPDKNDRYPGSGNCLGYSSGWWFDPACLSANLNGKYY 394
Db 407 HGTGAKQSSLLIH-CAD---FSTKADNDNCMC-KCALMLTGWGWFDPACPSNLNGMFY 461

QY 395 HQ-KYRGVRNGIFWGTGPGVSEAHFPGYKSSFKKAKMMIRPKHF 437
Db 462 TAGQNHGKLGINKWIKVFKGPS-----YSLRSTTMMIRPLDF 497
RESULT 15
US-09-162-437-4
Sequence 4, Application US/09162437
Patent No. 6166185
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,579
FILING DATE: 17-JAN-1995
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-4

Query Match 20.5%; Score 487; DB 3; Length 497;
Best Local Similarity 32.4%; Pred. No. le-36;
Matches 131; Conservative 59; Mismatches 136; Indels 78; Gaps 16;
QY 61 LPPLTIQLPKQFSRIE-----EVFKEVQNLKEIVNSLKKSCQDCKLQADDNGDPGRN 112
Db 145 LTDVETQVNLQTSRLIEQLLENSLSTYKLEKQLQQTNEILKIHE-----KN 191
QY 113 GLLLPSTGAPGEVDNRVRELESEVKNLSSELKNAKEEINVLHG-----RLEK-L 161

Db 192 SLL-----EHKILEME--GKHKELDTLKEKENLOGLVTRQTYIIQELEKOL 237
QY 162 NLVNMNNTIENVDSKVANLTFVNSLDGKCSK---CPSQEQIQSRPVQVHLYKDCSDYYA 218
Db 238 NRATTNN--SVLQKQOQLELMDTVHNLVNLCTKEVLLKGGKREEDKP-----FROCADVYQ 290
QY 219 IGKRSSEYRV-----TPDPKNSSFEVYCDMETMGCGWTVLQARLDGSTNFTTWQDYKAG 274
Db 291 AGFNKSGIYTYIINNMPFK-----KVFCNMDVNGGWTVIQHREDGSLDFQRCWKKEYKMG 346
QY 275 FGNLRREFWLGNDKIHLLTKSKEMILRIDLEFNGVELYALYQFVAVANEFLKYRLHVCN 334
Db 347 FGNPSGEYWLGNFEFAITSQRYMLRIELMDWEGNRAYSQYDRFHIGNEKONYRDLKLG 406
QY 335 YNGTAGDALRFNKHYNHDLKFEFTTPDKONDYPSGNCGLIYSSGWWFWDACL SANLNGKYY 394
Db 407 HTGTAGKQSSLIH-GAD---FSTKDADNDNCMC-KCALMLTGGWWFWDACGPSNLNGMFY 461
QY 395 HQ-KYRGVRNGIFWGTWPGVSEAHPGGYKSSPFKEAKMMIRPKHF 437
Db 462 TAGQNHGKLGKNGIKWHYFRGPS-----YSLRSTTMMIRPLDF 497

Search completed: February 27, 2001, 12:48:04
Job time: 30 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2001, 12:48:09 ; Search time 19.29 Seconds

(without alignments)
734.946 Million cell updates/sec

Title: US-09-442-143-2

Perfect score: 2378

Sequence: 1 MLANWYWLSSAVLATYGLF.....GYKSPFKAKMIRPKHFKP 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1853.5	77.9	432	1 FIBX_MOUSE	P12804 mus musculus
2	511.5	21.5	463	1 FIBB_CHICK	Q02020 gallus gall
3	481.5	20.2	453	1 FIBB_HUMAN	P04469 homo sapien
4	479.5	20.2	477	1 FIBB_PETMA	P02678 petromyzon
5	477.5	20.1	437	1 FIBG_HUMAN	P02679 homo sapien
6	471	19.8	468	1 FIBB_BOVIN	P02676 bos taurus
7	462	19.4	444	1 FIBG_BOVIN	P12799 bos taurus
8	461	19.2	438	1 FIBB_HUMAN	P02675 homo sapien
9	456	19.2	438	1 FIBG_XENLA	P17634 xenopus lae
10	454.5	19.1	479	1 FIBB_RAT	P14480 rattus norv
11	451	19.0	866	1 FIBA_HUMAN	P02671 homo sapien
12	446	18.8	282	1 FIBA_PARPA	P19477 parastichop
13	441	18.5	782	1 FIBA_RAT	P06399 rattus norv
14	428.5	18.0	432	1 FIBG_PETMA	P04115 petromyzon
15	427.5	18.0	741	1 FIBA_CHICK	P14448 gallus gall
16	419	17.6	445	1 FIBG_RAT	P02680 rattus norv
17	399	16.8	255	1 MFAL_HUMAN	P35083 homo sapien
18	397.5	16.7	4289	1 TENX_HUMAN	P22105 homo sapien
19	388	16.3	2201	1 TENA_HUMAN	P24821 homo sapien
20	386.5	16.3	1746	1 TENA_PIG	Q29116 sus scrofa
21	386	16.2	1808	1 TENA_CHICK	P10039 gallus gall
22	358.5	15.1	641	1 FIB2_PETMA	P33573 petromyzon
23	346.5	14.6	774	1 SCA_DROME	P21520 drosophila
24	185.5	7.8	129	1 MFAL_BOVIN	P55918 bos taurus
25	115	4.8	569	1 CISP_PLAFA	P25805 plasmodium
26	114.5	4.8	485	1 NOMR_RAT	O62609 rattus norv
27	114.5	4.8	964	1 QOYL_CAEEL	Q09560 caenorhabdi
28	114.5	4.7	1940	1 MYSE_RAT	P12847 rattus norv
29	112	4.7	1940	1 MYSE_HUMAN	P11055 homo sapien
30	107	4.5	1140	1 RA18_SCHPO	P53692 schizosacch
31	106.5	4.5	1664	1 RPAL_YEAST	P10964 saccharomyc
32	106	4.5	2245	1 MYSJ_DICDI	P54697 dictyosteli
33	105	4.4	362	1 RFL_AQUAE	O67032 aquifex aeo

RESULT 1

FIBX_MOUSE

ID FIBX_MOUSE STANDARD; PRT; 432 AA.

AC P12804;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PROTHROMBINASE PRECURSOR (FIBRINOGEN-LIKE PROTEIN) (CYTOTOXIC T-

DE LYMPHOCYTE SPECIFIC PROTEIN).

GN FIBLP OR FGL2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-CYTOTOXIC T-CELL;

RA MEDLINE=8717527; PubMed=3550794;

Koyama T., Hall L.R., Hasegawa S., Saito H.;

"Structure of a cytotoxic T-lymphocyte-specific gene shows a strong

homology to fibrinogen beta and gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).

[2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC STRAIN-BALB/CJ; TISSUE=PERITONEAL MACROPHAGE;

RA MEDLINE=95333285; PubMed=7609073;

Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,

Levy G.;

"Association of mouse fibrinogen-like protein with murine hepatitis

virus-induced prothrombinase activity.";

J. Virol. 69:5033-5038(1995).

CC -!- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.

CC -!- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC

CC T-CELLS.

CC -!- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS

CC VIRUS STRAIN 3 (MHV-3).

CC -!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF

CC THE BETA AND GAMMA CHAINS OF FIBRINOGEN.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL; M16238; AAA37624.1;

DR EMBL; M15761; AAA37624.1; JOINED.

DR EMBL; S78773; AAB34823.1;

DR PIR; A27447; A27447.

DR HSSP; P02671; IFZD.

DR MGI; MGI:103266; FGL2.

DR INTERPRO; IPR002181;

DR PFAM; PF00147; fibrinogen.C.1.

DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.

T-cell; Cytolysis; Blood coagulation; Signal.

KW

ALIGNMENTS

```

FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 432 PROTHROMBINASE.
FT DISULFID 206 235 BY SIMILARITY.
FT DISULFID 364 377 BY SIMILARITY.
FT CONFLICT 332 332 A -> G (IN REF. 2).
SQ SEQUENCE 432 AA; 48951 MW; 2B297F69CCB4A782 CRC64;

Query Match 77.9%; Score 1853.5; DB 1; Length 432;
Best Local Similarity 77.7%; Pred. No. 3.4e-119;
Matches 341; Conservative 42; Mismatches 49; Indels 7; Gaps 4;

Qy 1 MRLANWYLSAVLATYGLVANNETEIKDERAKDQVPRLESRGKEEAGECYPQVS 60
Db 1 MRLPGWLWLSAVLAACR-AVEEHLTEGLEDAQAACPARLEGSGRC-EGSQCPFLT 58
Qy 61 LPPLTIQLPKQFSRETEVEFKEVQNLKEIYVNSLKKSCQDCKLQADDDGPRNGLLPSTG 120
Db 59 LPTLTILQPRQGSWEELVKEVRLKEAVDSLKKSCQDCKLQADDDHRDPGGNG----GNG 114
Qy 121 APGEYGDNRVRESEVANKLSSELNKAKEEINVHLGRLEKLNLVNMMNIENYVDSKVANL 180
Db 115 AE-TAEDSRVQELSEVQVNSLKKSCQDCKLQADDDHRDPGGNG----GNG 114
Qy 181 TFVNSLDGKCKSPSQEQIQSRPOVHLLYKDCSDYIAGKRSSYRTVTPDPKNSFEV 240
Db 174 TVVNSLDGKCKSPSQEQIQSRPOVHLLYKDCSDYIAGKRSSYRTVTPDPKNSFEV 233
Qy 241 YCDMETGSGWTVLQARLDGSGNFTFTWQDYKAGFCNLRREFWLGNDKTHLLTKSEMIL 300
Db 234 YCDMETGSGWTVLQARLDGSGNFTFTWQDYKAGFCNLRREFWLGNDKTHLLTKSEMIL 293
Qy 301 RIDLDFNGVELYALYDQFYVANEFLKYLHVGNYGTAGDALRFNKHYNHDLKFTTTPD 360
Db 294 RIDLDFNGVELYALYDQFYVANEFLKYLHVGNYGTAGDALRFNKHYNHDLKFTTTPD 353
Qy 361 KNDRYPSGNCGLYSSGWWFDFACLSANLNGYKHQYKRGVNRGIFWGTWPGVSEAHPGG 420
Db 354 RNDRYPSGNCGLYSSGWWFDFACLSANLNGYKHQYKRGVNRGIFWGTWPGVSEAHPGG 413
Qy 421 YKSSFEAKMMTRPKFKP 439
Db 414 YKSSFEAKMMTRPKFKP 432

RESULT 2
FIBB_CHICK
ID FIBB_CHICK STANDARD; PRT; 463 AA.
AC Q02020;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN BETA CHAIN PRECURSOR (FRAGMENT).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=91182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
RT cleavage site.";
RL Biochemistry 30:3290-3294(1991).
RC FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

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CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -----
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CC -----
CC EMBL; M58514; AAA48770.1; -.
CC PIR; A38463; A38463.
CC HSSP; P02675; 1FZ8.
CC INTERPRO; IPR002181; -.
CC PFAM; PF00147; fibrinogen_C; 1.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfatation.
CC FT NON_TER 1 1 FIBRINOPEPTIDE B.
CC PEPTIDE <1 17 FIBRINOPEPTIDE B.
CC CHAIN 18 463 FIBRINOGEN BETA CHAIN.
CC MOD_RES 5 5 SULFATATION (BY SIMILARITY).
CC SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
CC FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
CC FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
CC FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
CC FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
CC FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
CC FT DISULFID 205 289 BY SIMILARITY.
CC FT DISULFID 215 244 BY SIMILARITY.
CC FT DISULFID 397 410 BY SIMILARITY.
CC FT CARBOHYD 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 463 AA; 52678 MW; 2044CD49BA79EC7B CRC64;

Query Match 21.5%; Score 511.5; DB 1; Length 463;
Best Local Similarity 30.4%; Pred. No. 8.1e-28;
Matches 137; Conservative 71; Mismatches 154; Indels 89; Gaps 16;

Qy 31 KDERAKDQVPRLESRGK-----EEAGE-CPYQVSLPPLTQLPKQFSRIEVEFKEVQN- 84
Db 51 QDKQAMKGPPIYPDAGGCKHPDELGVLCPTGCE---LQTTLLKQEKTVKPVRLDKDR 107
Qy 85 -----LKEIVNSLKKSCQDCKLQADDDGPRNGLLPSTGAPGEYGDNRVRELE 134
Db 108 VAKFSDTSTTMYQVYVNMIDNKLVTQKQKD-----NDIILSEYNTMELHYNVIK--D 159
Qy 135 SEVNLKLSSELNKAKEEINVHLGRLEKLNLVNMMNIENYVDSKVANLTFVNSLDGKCKSC 194
Db 160 NLDNNIPSSLRLRAVDSLHKKIQL-----ENAIATQT-----DYCRSPC 201
Qy 195 PSQIQIQRVQVHLLYKDCSDYIAGKRSSYRTVTPDPKNSFEVCDMETGSGWTVL 254
Db 202 -----VASCNIPVSGRECEDIYRKGETSEMYIIQDPFTTPYRVYCDMETGSGWTVL 256
Qy 255 QARLDGSGNFTFTWQDYKAGFCNLR-----EFLGNDKTHLLTKSEMILRID 303
Db 257 QNRDGSVNFGRADWEYKRGFGNIAKSGGKCYCDTPGEYWLGNDKISQLTKIGTKVLIE 316
Qy 304 LEDPNGVELYALYDQFYVANEFLKYLHVGNYGTAGDALR--FNKHYN-----HDLK 354
Db 317 MEDWNGDKVSAIYGGFTIHNEGNYQLSVSNYKGNAGNLMEGASQLYGERNTMTIHNGM 376
Qy 355 FFTTPDKNDRY-----PSGNCGLYSSGWWFDFACLSANLNGKY-----HQYRGVNR 403
Db 377 YFSTYDRDNDGWLTDPRKQCKSKEDGGGWTFNRCHAANPNRGYWGTYSWDMAKHGPD 436
Qy 404 GIFWGTWPGVSEAHPGGYKSSFEAKMMIRP 434

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Db 437 GIVMWNKG-----SWY--SMKMSMKIRP 459
RESULT 3
FIBH_HUMAN
ID FIBH_HUMAN STANDARD; PRT; 453 AA.
AC P04469; P04470;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE FIBRINOGEN GAMMA-B CHAIN PRECURSOR (FIBRINOGEN GAMMA').
GN FGG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85252774; PubMed=2990550;
RA Rixon M.W., Chung D.W., Davie E.W.;
RT "Nucleotide sequence of the gene for the gamma chain of human
RT fibrinogen."
RL Biochemistry 24:2077-2086(1985).
RN [2]
RX CHROMATOGRAPHIC COMPARISON OF GAMMA-A AND GAMMA-B CHAINS.
RP MEDLINE=81054908; PubMed=6933547;
RA Wolfenstein-Todel C., Mosesson M.W.;
RT "Human plasma fibrinogen heterogeneity: evidence for an extended
RT carboxyl-terminal sequence in a normal gamma chain variant
RT (gamma')."
RL J. Biol. Chem. 259:12826-12830(1984).
RN [4]
RP SEQUENCE OF 411-453.
RX MEDLINE=82068993; PubMed=7306501;
RA Wolfenstein-Todel C., Mosesson M.W.;
RT "Carboxy-terminal amino acid sequence of a human fibrinogen
RT gamma-chain variant (gamma')."
RL Biochemistry 20:6146-6149(1981).
RN [5]
RP SULFATATION.
RX MEDLINE=91369960; PubMed=1892842;
RA Farrel D.H., Mulvihill E.R., Huang S., Chung D.W., Davie E.W.;
RT "Recombinant human fibrinogen and sulfation of the gamma' chain."
RL Biochemistry 30:9414-9420(1991).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- ALTERNATIVE PRODUCTS: THIS CHAIN DIFFERS FROM THE GAMMA-A CHAIN
CC AT RESIDUES 434-437 FOLLOWED BY 16 ADDITIONAL RESIDUES OF THE
CC CARBOXYL END. THESE DIFFERENCES ARE PRODUCED BY AN ALTERNATE
CC SPLICING OF THE MRNA IN WHICH THE EIGHTH (LAST) INTRON IS NOT
CC REMOVED.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -!- MISCELLANEOUS: THE GAMMA-B CHAIN IS PRESENT IN ABOUT 10% OF THE
CC FIBRINOGEN MOLECULES IN PLASMA BUT ABSENT FROM THOSE IN THE
CC PLATELETS.

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CC -----
DR EMBL; M10014; AAB59530.1; -
DR EMBL; X02415; -; NOT_ANNOTATED_CDS.
DR EMBL; K02569; AAB52430.1; -
DR PIR; A03126; FGHUGB.
DR HSSP; P02679; LFZB.
DR MIN; 134850; -
DR INTERPRO; IPR002181; -
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma;
KW Alternative splicing; Sulfatation; Signal.
FT SIGNAL 1 26
FT CHAIN 27 453 FIBRINOGEN GAMMA-B CHAIN.
FT CARBOHYD 78 78 N-LINKED (GLCNAC. .).
FT DISULFID 34 34 INTERCHAIN (WITH C-35').
FT DISULFID 35 35 INTERCHAIN (WITH C-34').
FT DISULFID 45 45 INTERCHAIN (WITH C-110 IN BETA).
FT DISULFID 49 49 INTERCHAIN (WITH A-64 IN ALPHA).
FT DISULFID 161 161 INTERCHAIN (WITH C-227 IN BETA).
FT DISULFID 165 165 INTERCHAIN (WITH C-180 IN ALPHA).
FT DISULFID 179 208
FT DISULFID 352 365
FT CA_BIND 341 355
FT SITE 400 422
FT
FT POLYMERIZATION SITE, BINDING TO THE
FT AMINO END OF ALPHA-CHAIN OF ANOTHER
FT FIBRIN MONOMER.
FT BINDING 424 424 CROSS-LINK TO 432-LYS AND 424-GLN.
FT BINDING 432 432 CROSS-LINK TO 432-LYS AND 424-GLN.
FT MOD_RES 444 444 SULFATATION (PROBABLE).
FT CONFLICT 435 435 R -> Y (IN REF. 4).
FT CONFLICT 448 448 Y -> R (IN REF. 4).
SQ SEQUENCE 453 AA; 51496 MW; FA647C5E85A2013A CRC64;
Query Match 20.2%; Score 481.5; DB 1; Length 453;
Best Local Similarity 29.3%; Pred. No. 8.7e-26;
Matches 139; Conservative 59; Mismatches 177; Indels 99; Gaps 17;
QY 8 WLSSAVLATYGVLVVANNETEIEIKDERAKDVCPRLESRGKCEAGECPYQVSLPLTIQ 67
Db 19 FLSTCVV-----YVATRDNCILDERGSGYCPT-----TCGIADFLSTYQTK 61
QY 68 LPKQFSRIEEVFEVQNLKEIVNSLKKSCQCKLQADDGDPGRNGLLLPSTGAPGEVGD 127
Db 62 VDKDLQSLDELHQQENKTSVKQLIKA-----IQLTYNPDESSKPNMIDATLKSRLML 116
QY 128 NRVRELESEVNKLSELKNAKEEINVLHGRLEKMLVNMNIENYVDSKVANLTFVNSL 187
Db 117 EEIMKYEASILTTHDSSTRYLQE-----IYNSNN-----QKIVNLKEKVAQL 157
QY 188 DGKCSKPSQEQIQSRPVQVHLLYKDCSDYVYAIKGRSSSTYRVTDPKSSSEVYCDMETM 247
Db 158 EAQCEP-CKDTVQ---IHDITGDCQDIANKGAKQSGLYFIKPKANQOFLVYCEIDGS 213
QY 248 GGGWTVLQARLDGSTNFTTRTWQDYKAGFGNL-----RREFWLGNDKIHLLTSKEM--ILR 301
Db 214 GNGWTVFQKRLDGSVDKFKNNIQYKEGFGHLSPGTTEFWLGNKXIHLLTSQSAIPYALR 273
QY 302 IDLEDFNGVELYALDQPYVANEFLKYLHVGNY--NGTAGDAL--RFNKHYNHDLKFFTT-- 357
Db 274 VELEDWNGRTSTADYAMFKVGPPEADKYRLTYAYFAGGDAGDAFDGDFGDDPSDKFFTS 333
QY 358 -----TPDKNDNDRYPSGNCGLYSSGWFWDACLSANLNGKYH-----QKYRGVNG 404

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FT	DISULFID	212	212	INTERCHAIN (WITH THE ALPHA CHAIN)	
FT				(BY SIMILARITY).	
FT	DISULFID	216	216	INTERCHAIN (WITH THE GAMMA CHAIN)	
FT				(BY SIMILARITY).	
FT	DISULFID	220	304	BY SIMILARITY.	
FT	DISULFID	230	259	BY SIMILARITY.	
FT	DISULFID	412	425	BY SIMILARITY.	
FT	SEQUENCE	477 AA;	54270 MW;	B8A95E7E32D09D18 CRC64;	

Query Match	20.2%;	Score 479.5;	DB 1;	Length 477;
Best Local Similarity	29.2%;	Pred. No. 1.3e-25;		
Matches 131;	Conservative 66;	Mismatches 138;	Indels 113;	Gaps 15;

QY	29	EIKDERAKDVCVPRLESRGKCEAG	CPYOVSLPPLTIQLPKQFSRIEEVFKEVQNLKEI	88
DBb	100	ELREELLKQDPVR-----	YKISMLK-----	QNLTYF 126
QY	89	VNSLKSKCDQCKLQADDNGDPGRNGLL	PLSTGAPGVDGNRVRELESEVNSKLSELKNAK	148
DBb	127	INSFDR-----	MASDSNTLKQN-----	VQTLRRRLNSRSTHYNQAQ 162
QY	149	EEINVLHGLEKLNLMNMIENYVDSKAN	LVFNLSLDGKCSK----	CPSQEQIQSRP 204
DBb	163	KEI---ENRYKEYKI-----	RIESTVAGSLRSMKSVLEHLRAKQMREEA	IKTOKELCASP 215
QY	205	-----VQHLIYKDCDYAIGKRSS	ETRYVTPDKNSSFEVYCDMETMGGWTVLOARL	258
DBb	216	CTVNCRPVVSVMHCEDIYRNGRTSEAY	IQDPLFSEPKYVFCDMESHGGGWTVVQNRV	275
QY	259	DGSTNFTRWODYKAGFGNLR-----	REFVLGNDKIHLLTKSKEMILRIDLEDF	307
DBb	276	DGSSNARDWNTYKAEFGNIAFGNGK	SICNIPGEVWLGTKTVHOLTQKHTQOVLFDM	SDW 335
QY	308	NGVELYALYDQFVANEFLYRLHGVN	YNGTAGDAL-----	RFNKHYN-HDLKFTTT 358
DBb	336	EGSSVYAOYASFRENPAQGYRLWVED	YSGNAGNALLEGATQLMGDNRTMTIHNGM	QFST 395
QY	359	PKDKNDRY---PSGNGCLYYSGW	WFDACL SANLNGKY-----	HOKYRGVRNGIFW 407
DBb	396	FDRDNDWNPDPTKHCSDREDAGGW	TNRCHAAANPGRYWGGIYTKEQADY	GTDDGVVW 455
QY	408	GTWPGVSEAHPGGYKSSFKFEAK	MMIRPK 435	
DBb	456	MNWKG-----SWY--	SMRQWAMKLRPK 475	

RESULT 5	
FIBG.HUMAN	
ID	FIBG.HUMAN
AC	STANDARD;
AD	PRT;
CD	437 AA.
DT	21-JUL-1986 (Rel. 01, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-JUL-1999. (Rel. 38, Last annotation update)
DE	FIBRINOGEN GAMMA-A CHAIN PRECURSOR.
GN	FGG.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=85252774; PubMed=2990550;
RX	Rixon M.W., Chung D.W., Davie E.W.;
RA	"Nucleotide sequence of the gene for the gamma chain of human
RT	fibrinogen."
RL	Biochemistry 24:2077-2086(1985).
RN	[2]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=83283434; PubMed=6688357;
RT	Chung D.W., Chan W.-Y., Davie E.W.;
RA	"Characterization of a complementary deoxyribonucleic acid coding for
RL	the gamma chain of human fibrinogen."
RL	Biochemistry 22:3250-3256(1983).

RN [3]
 RP SEQUENCE OF 27-437.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 structural variants.";
 RL (In) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [4]
 RP SEQUENCE OF 75-286 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=92119334; PubMed=1685103;
 RA Marchetti L., Zanelli T., Malcovati M., Tenchini M.L.;
 RT "Polymorphism of the human gamma chain fibrinogen gene.";
 RL DNA Seq. 1:419-422(1991).
 RN [5]
 RP SEQUENCE OF 285-437 FROM N.A.
 RX MEDLINE=85030379; PubMed=602346;
 RA Fornace A.J. Jr., Cummings D.E., Comeau C.M., Kant J.A.,
 RA Crabtree G.R.;
 RT "Structure of the human gamma-fibrinogen gene. Alternate mRNA
 RT splicing near the 3' end of the gene produces gamma A and gamma B
 RT forms of gamma-fibrinogen.";
 RL J. Biol. Chem. 259:12826-12830(1984).
 RN [6]
 RP SEQUENCE OF 209-270 FROM N.A.
 RX MEDLINE=84069777; PubMed=6689067;
 RA Imam A.M.A., Eaton M.A.W., Williamson R., Humphries S.;
 RT "Isolation and characterization of cDNA clones for the A alpha- and
 RT gamma-chains of human fibrinogen.";
 RL Nucleic Acids Res. 11:7427-7434(1983).
 RN [7]
 RP REVIEW, AND DISULFIDE BONDS
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [8]
 RP DISULFIDE BONDS
 RA Doolittle R.F., Takegi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [9]
 RP DISULFIDE BONDS
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [10]
 RP QUATERNARY STRUCTURE, AND DISULFIDE BONDS.
 RX MEDLINE=83231465; PubMed=6860649;
 RA Hoeprich P.D., Doolittle R.F.;
 RT "Dimeric half-molecules of human fibrinogen are joined through
 RT disulfide bonds in an antiparallel orientation.";
 RL Biochemistry 22:2049-2055(1983).
 RN [11]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [12]
 RP POLYMERIZATION SITE.
 RX MEDLINE=85014892; PubMed=6592597;
 RA Horwitz B.H., Varadi A., Scheraga H.A.;
 RT "Localization of a fibrin gamma-chain polymerization site within
 RT segment Thr-374 to Glu-396 of human fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5980-5984(1984).
 RN [13]

RP POLYMERIZATION SITE.
 RX MEDLINE=81142375; PubMed=6451630;
 RA Olexa S.A., Budzynski A.Z.;
 RT "Localization of a fibrin polymerization site.";
 RL J. Biol. Chem. 256:3544-3549(1981).
 RN [14]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE=84203545; PubMed=6326808;
 RA Kloczewiak M., Timmons S., Lukas T.J., Hawiger J.;
 RT "Platelet receptor recognition site' on human fibrinogen. Synthesis
 RT and structure-function relationship of peptides corresponding to the
 RT carboxy-terminal segment of the gamma chain.";
 RL Biochemistry 23:1767-1774(1984).
 RN [15]
 RP PLATELET AGGREGATION SITE.
 RX MEDLINE=84185664; PubMed=6325435;
 RA Ploew E.F., Srouji A.H., Meyer D., Marguerie G., Ginsberg M.H.;
 RT "Evidence that three adhesive proteins interact with a common
 RT recognition site on activated platelets.";
 RL J. Biol. Chem. 259:5388-5391(1984).
 RN [16]
 RP CALCIUM-BINDING SITE.
 RX MEDLINE=85261382; PubMed=3160702;
 RA Dang C.V., Ebert R.F., Bell W.R.;
 RT "Localization of a fibrinogen calcium binding site between
 RT gamma-subunit positions 311 and 336 by terbium fluorescence.";
 RL J. Biol. Chem. 260:9713-9719(1985).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE=97169449; PubMed=9016719;
 RA Yee V.C., Pratt K.P., Cote H.C.F., le Trong I., Chung D.W.,
 RA Davie E.W., Stenkamp R.E., Teller D.C.;
 RT "Crystal structure of a 30 kDa C-terminal fragment from the gamma
 RT chain of human fibrinogen.";
 RL Structure 5:125-138(1997).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 169-437.
 RX MEDLINE=9735771; PubMed=9207064;
 RA Pratt K.P., Cote H.C.F., Chung D.W., Stenkamp R.E., Davie E.W.;
 RT "The primary fibrin polymerization pocket: three-dimensional
 RT structure of a 30-kDa C-terminal gamma chain fragment complexed with
 RT the peptide Gly-Pro-Arg-Pro.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7176-7181(1997).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 114-432.
 RX MEDLINE=97472408; PubMed=9332333;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its
 RT crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 114-432.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [22]
 RP VARIANT ASAH1.
 RX MEDLINE=89214687; PubMed=2496144;
 RA Yamazumi K., Shimura K., Terukina S., Takahashi N., Matsuda M.;
 RT "A gamma methionine-310 to threonine substitution and consequent N-
 RT glycosylation at gamma asparagine-308 identified in a congenital
 RT dysfibrinogenemia associated with posttraumatic bleeding, fibrinogen
 RT Asahi.";
 RL J. Clin. Invest. 83:1590-1597(1989).


```

Db 321 GDSSDKFTSHNGMFWSDNDXY-DGNCAEQVIGWMMKCHAGHNGVYQGGTY 379
QY 396 ---QYRGVNRGIFWGTGPGVSEAHGGYKS-----SPKEAKMMIRP 434
Db 380 SKTSTPNGYDNGIIMATW-----KSRWYSMKKTTMKIIP 413

RESULT 8
FIBB_HUMAN
ID FIBB_HUMAN STANDARD; PRT; 491 AA.
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FIBRINOGEN BETA CHAIN PRECURSOR.
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9134740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RL fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic
RL deoxyribonucleic acid for the beta chain of human fibrinogen.";
RL Biochemistry 22:3244-3250(1983).
RN [3]
RP SEQUENCE FROM N.A.
RX Chung D.W., Harris J.E., Davie E.W.;
RL (In) Chien S. (eds.);
RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
RN Plenum Press, New York (1991).
RN [4]
RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RN structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RN Pergamon Press, Oxford (1980).
RN [5]
RP SEQUENCE OF 31-491.
RX MEDLINE=79124640; PubMed=420779;
RA Watt K.W.K., Takagi T., Doolittle R.F.;
RT "Amino acid sequence of the beta chain of human fibrinogen.";
RL Biochemistry 18:68-76(1979).
RN [6]
RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
RX MEDLINE=76225080; PubMed=936108;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL Thromb. Res. 8:639-658(1976).
RN [7]
RP SEQUENCE OF 1-38 FROM N.A.
RX MEDLINE=87146483; PubMed=3029722;
RA Huber P., Dalmon J., Courtols G., Laurent M., Assouline Z.,
RN Marguerie G.;
RT "Characterization of the 5'-flanking region for the human fibrinogen
RL beta gene.";
RL Nucleic Acids Res. 15:1615-1625(1987).
RN [8]
RP SEQUENCE OF 31-44.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).

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RN [9]
RP REVIEW, AND DISULFIDE BONDS.
RX MEDLINE=83254370; PubMed=6575689;
RA Henschen A., Lottspeich F., Kehl M., Southan C.;
RT "Covalent structure of fibrinogen.";
RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=77245999; PubMed=891553;
RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
RT "Primary structure of human fibrinogen. Characterization of
RN disulfide-containing cyanogen-bromide fragments.";
RL Eur. J. Biochem. 77:595-610(1977).
RN [11]
RP DISULFIDE BONDS.
RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
RT "The structures of fibrinogen and fibrin.";
RL (In) Magnusson S., Ottesen M., Foltmann B., Dano K.,
RL Neurath H. (eds.);
RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
RN Pergamon Press, New York (1978).
RN [12]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RT "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
RX MEDLINE=97472408; PubMed=933233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RN crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RN different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [15]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RN fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [16]
RP VARIANT BALTIMORE-2.
RX MEDLINE=89058942; PubMed=3194892;
RA Schneizer C.H., Ebert R.F., Bell W.R.;
RT "A polymorphism at B beta 448 of fibrinogen identified during
RN structural studies of fibrinogen Baltimore II.";
RL Thromb. Res. 52:173-177(1988).
RN [17]
RP VARIANT ISE.
RX MEDLINE=91208409; PubMed=2018836;
RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
RA Asakura S., Shirakawa S.;
RT "A new congenital abnormal fibrinogen Ise characterized by the
RN replacement of B beta glycine-15 by cysteine.";
RL Blood 77:1958-1963(1991).
RN [18]
RP VARIANT NAPLES.
RX MEDLINE=92340664; PubMed=1634610;
RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
RT "Molecular basis of fibrinogen Naples associated with defective
RN thrombin binding and thrombophilia. Homozygous substitution of B beta
RL 68 Ala-->Thr.";
RL J. Clin. Invest. 90:238-244(1992).
RN [19]

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RP VARIANTS ILMUIDEN AND NIJMEGEN.
RX MEDLINE=9222809; PubMed=1565641;
RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
RT Kerst A.F.J.A., Lord S.T.;
RA "Abnormal fibrinogens ILMuiden (B beta Arg44-->Cys) and Nijmegen (B
RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
RT complexes.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
RN [20]
RP VARIANT NEW YORK-1.
RX MEDLINE=85157605; PubMed=3156856;
RA Liu C.Y., Koehn J.A., Morgan F.J.;
RT "Characterization of fibrinogen New York 1. A dysfunctional
RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
RT exon 2 of the gene.";
RL J. Biol. Chem. 260:4390-4396(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COLLS, WHICH
CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
CC ENDS OF THE ALPHA CHAINS.
CC -!- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC
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CC
DR EMBL; J00129; AAA52429.1; -
DR EMBL; J00131; AAA98115.1; -
DR EMBL; J00130; AAA98115.1; JOINED.
DR EMBL; J00132; AAA98116.1; -
DR EMBL; J00133; -; NOT_ANNOTATED_CDS.
DR EMBL; X05018; CAA28674.1; -
DR EMBL; M4983; AAA18024.2; -
DR EMBL; M26877; AAA52445.1; -
DR EMBL; M26876; AAA52445.1; JOINED.
DR PIR; B43568; FGHUB.
DR PDB; 1FZA; 03-DEC-97.
DR PDB; 1FZB; 03-DEC-97.
DR PDB; 1FZC; 14-OCT-98.
DR PDB; 1FEZ; 08-JUN-99.
DR PDB; 1FEF; 08-JUN-99.
DR PDB; 1FZG; 08-JUN-99.
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DR MIM; 134830; -
DR INTERPRO; IPR002181; -
DR PFAM; PF00147; fibrinogen_C; 1.
Query Match 19.4%; Score 461; DB 1; Length 491;
Best Local Similarity 28.7%; Pred No. 2.4e-24;
Matches 133; Conservative 57; Mismatches 161; Indels 112; Gaps 14;
QY 27 TPEIKDERAKDVCPRVLESGRKEEAGE-----CPYQVSLPPLTIQLPKOF-SRIIEVFK 80
DB 81 TQKKVERKAPDA-----GGCLHADPDGLVLCPTGCGQLQALLQOERPIRNSVDLENN 132

QY 81 EVQNLKEIVNS-----LKKSCQDCKLQADDNGDPGRNGLLLPSTGAPGEVGDNRVREL 133
DB 133 NVEAVSQSSSSSQFYMYLLKDLQKQKQVKN----- 165
QY 134 ESEVKNLSSELKNAKEEINVLGRLEKLNLMNMIENIYVDSKVANLTFVNSLDGKCSK 193
DB 166 ENVVNEYSSE-----LEKHQLYIDETVNSNIPNLRLVRLSILENLSKIQK 211
QY 194 CPSQEQIO-----SRPQHLIYKDCSDYYAIGKRSSSEYRYVTPDPKNSSEFVYCD 243
DB 212 LESDVAQMEYCRTPCTSCNIPVVSGRCEEIIIRKGETSEMYLIQDSSSVKPRVYCD 271
QY 244 METGGGTVTLQARLDGSTNFTRTWQDYKAGFNG-----LRREFWLGNKDIHL 291
DB 272 MNTGGGTVTLQARLDGSTNFTRTWQDYKAGFNG-----LRREFWLGNKDIHL 331
QY 292 LTKSKEMILRDLDFNGVELYALYDQFYVANEFLKYRLHVGNYNGTAGDALR----- 344
DB 332 LTRMGPTELLIEEMEDWKGVKAHYGGFTVQNEANKYQISVKNKYRTAGNALMDGASQLM 391
QY 345 -FNKHYN-HDLKFFETTPDKNDRY-----PSGNCGLIYSGWFWDFACLSANLNGKY - 394
DB 392 GENRTMTIHNGMFTSTYDRDNGWLTSDPRKQCSKEDGGGWMYNRCHAANPNGRYWGQ 451
QY 395 ---HQYRGVRNGIFWGTWPGVSEAHPGYKSSFKKAKMIRP 434
DB 452 YTWDAKHGTDGTVVMMWKG-----SWY--SMRKMSMKIRP 486
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AC P17634;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-AUG-1990 (Rel. 15, Last sequence update)
DE FIBRINOGEN GAMMA CHAIN PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90241882; PubMed=2334684;
RA Pastori R.L., Moskaitis J.E., Smith L.H. Jr., Schoenberg D.R.;
RT "Estrogen regulation of Xenopus laevis gamma-fibrinogen gene
RT expression.";
RL Biochemistry 29:2599-2605(1990).
RN [2]
RP SEQUENCE OF 1-58 FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=91146806; PubMed=2289632;
RA Bhattacharya A., Shepard A.R., Moser D.R., Holland L.J.;
RT "Isolation and characterization of cDNA clones for the gamma subunit
RT of Xenopus fibrinogen, the product of a coordinately regulated gene
RT family.";
RL Mol. Cell. Endocrinol. 72:213-220(1990).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -


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FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 219 304 BY SIMILARITY.
FT DISULFID 229 258 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
FT CONFLICT 439 439 L -> O (IN REF. 5).
FT CONFLICT 441 441 S -> T (IN REF. 5).
FT CONFLICT 445 445 S -> A (IN REF. 5).
FT CONFLICT 467 467 R -> K (IN REF. 5).
FT CONFLICT 475 475 V -> F (IN REF. 5).
SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3E0BC0 CRC64;

Query Match 19.1%; Score 454.5; DB 1; Length 479;
Best Local Similarity 31.2%; Pred. No. 6.4e-24;
Matches 116; Conservative 46; Mismatches 135; Indels 75; Gaps 10;

QY 128 NRVRELESEVN-----KLSSELKNAKEEINVHGRLEKLNIVNM 166
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Db 173 ETVNDNIPLNRLVRSILEDLSRKQKLESIDISAQTEYCHTPTVCNCPV--VSKECE 230
QY 215 DYATGKRSESTYRTPPKNSFFVYCDMETMGGWTLQARLDGSTNFTRTWQDYKAG 274
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Db 291 FGNATNEDTKYCYGLPEYWLGNDKISQLTRIGPTTELLIEMEDMKGRVKAHYGFTWQ 350
QY 323 NEFLKRLHVGNNGTAGDALAR-----FNKHVN-HDLKFFTPDKNDRY----PSG 369
Db 351 TEANKYQSVNKKYKTAGNALMEGASQLVNGENTHTIHNCFEFSYDRNDGQWTTDPKR 410
QY 370 NGLYSSGWFDACLSANLKKY-----HQRYGVNRNGIFWGTWPGVSEAHFPGYK 422
Db 411 QCSKEDGGWVYNRCHAANPNRGYVWGGLYSWDMSKHGTDGCVVWNWKG-----SWI- 463
QY 423 SSFREAKMIRP 434
Db 464 -SMRRMSMKIRP 474

RESULT 11
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ID FIBA_HUMAN STANDARD; PRT; 866 AA.
AC P02671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
GN FGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A. (ALPHA-E FORM).
RX MEDLINE=93090725; PubMed=1457396;
RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA Roy S.N., Redman C.M., Grieninger G.
RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits."
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).

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RA Chung D.W., Grieninger G.;
RL (In) Ebert R.F. (eds.);
RL Index of variant human fibrinogens, pp.13-24, CRC Press,
RL Boca Raton (1994).
RN [3]
RP SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
RC TISSUE=LIVER;
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen."
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [4]
RP SEQUENCE FROM N.A. (ALPHA FORM).
RX MEDLINE=83247396; PubMed=6575389;
RA Kant J.A., Lord S.T., Crabtree G.R.;
RT "Partial mRNA sequences for human A alpha, B beta, and gamma
RT fibrinogen chains: evolutionary and functional implications."
RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN [5]
RP SEQUENCE OF 1-629 FROM N.A.
RX MEDLINE=83283432; PubMed=6688355;
RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the alpha chain of human fibrinogen."
RL Biochemistry 22:3237-3244(1983).
RN [6]
RP SEQUENCE OF 20-629.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT structural variants."
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [7]
RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX MEDLINE=80088231; PubMed=518846;
RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Overlapping sequences providing the complete sequence."
RL Biochemistry 18:5410-5416(1979).
RN [8]
RP SEQUENCE OF 110-156 FROM N.A.
RX MEDLINE=84069777; PubMed=6689067;
RA Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT "Isolation and characterisation of cDNA clones for the A alpha- and
RT gamma-chains of human fibrinogen."
RL Nucleic Acids Res. 11:7427-7434(1983).
RN [9]
RP SEQUENCE OF 605-644 FROM N.A. (ALPHA FORM).
RX MEDLINE=83254384; PubMed=6575700;
RA Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT "Cloning of fibrinogen genes and their cDNA."
RL Ann. N.Y. Acad. Sci. 408:449-456(1983).
RN [10]
RP SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates."
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [11]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=80088230; PubMed=518845;
RA Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Exact location of cross-linking acceptor sites."
RL Biochemistry 18:5405-5410(1979).
RN [12]
RP CROSS-LINKING ACCEPTOR SITES.
RX MEDLINE=78130085; PubMed=632262;
RA Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT "Localization of the alpha-chain cross-link acceptor sites of human
RT fibrin."
RL J. Biol. Chem. 253:2184-2195(1978).

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"Fibrinogen Lima: a homozygous dysfibrinogen with an A alpha-arginine-141 to serine substitution associated with extra N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel formation but normal fibrin-facilitated plasminogen activation catalyzed by tissue-type plasminogen activator.;" J. Clin. Invest. 90:67-76(1992).

[241]
RN VARIANT CARACAS-2.
RP MEDLINE=91268018; PubMed=1675636;
RA Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA Arocha-Pinango C.L., Matsuda M.;
RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a
RT dysfibrinogen, fibrinogen Caracas II, characterized by impaired
RT fibrin gel formation.;"
RL J. Biol. Chem. 266:11575-11581(1991).
RN [25]
RN VARIANT DUSART.
RP MEDLINE=93232289; PubMed=8473507;
RA Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mossesson M.W.,
RA D'orio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA Caen J.P.;
RT "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and
RT its association with abnormal fibrin polymerization and
RT thrombophilia.;"
RL J. Clin. Invest. 91:1637-1643(1993).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL MODULE.
CC DIVERGING FROM THIS MODULE ARE 2 THREE-CHAIN COILED COILS, WHICH

Query Match 19.0%; Score 451; DB 1; Length 866;
Best Local Similarity 32.5%; Pred. No. 2.4e-23;
Matches 136; Conservative 51; Mismatches 137; Indels 94; Gaps 21;

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DB 476 KEY--TREVVIS--EGSDCP-EAMDGLTSGIGTLGDFRHRHPDEAFTASTGTFF 530
QY 118 STGAP--GEVGDNRVRESEVANKLSSELKNAKEINVLHGRLE-----KLN 162
DB 531 GFTSPMLGEF---VSTESRGSE-SGIFTKRESSHHPCIAEFPSRGKSSYSKQFTS 585
QY 163 LVNMNIENYVDSKANLTFVWNS-LDGKSKCPSQIQOSRPVQHLIYKDSY----YA 218
DB 586 STSYNRGSDSTFESKYSKMADEAGSEADHEGTHSTKRGHAKSRPV-----RDCDVLQTHP 640
QY 219 IGRSSETYRTVPDPKNSFEVYCDMTGSGTTLQARLDGNSFTRTWQDYKAGFNL 278
DB 641 SGTQSG-IFNKLPGSKSIFSYCDQTSIGWLLIQORWDGSLNFRTWQDYKRGFGL 699
QY 279 ----REFVLGNDKIHLITTSKEMILIDLEDFNGVELYALYDQFYVANEFLKYRLHVG 334
DB 700 NDEGEGEFGLNDYLHLTQ-RGSLVRLVELEDWAGNEAYAEY-HFRVGEAEGLQVSS 757
QY 335 YNQTADAL-----RPNKHYNHDLKFTFTDPKNDPRYPSGNCGLIYSSGWWFACL 385
DB 758 YEGTAGDALLIEGSVEEGAETYSHNMQ---FSTPDRADQWEE-NCAEVYGGGWWYNNQC 813
QY 386 SANLNGKY-----HQRGVRNGIFGTWGPVSEAHPGGYKSKFKAEMWIRP 434
DB 814 AANLNGIYPGGSYDPRNNSPYE-IENGVMVMSRPGAD-----YSLRAVRMKIRP 862

RESULT 12
FIBA_PARPA STANDARD; PRF; 282 AA.
ID FIBA_PARPA
AC P19477;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
OS Parastichopus parvimensis (Sea cucumber).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Holothuroidea; Aspidochiroptera; Aspidochiroptida; Stichopodidae;
OC Parastichopus.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=SOFT TISSUES;
RX MEDLINE=90192754; PubMed=2315305;
RA Xu X., Doolittle R.F.;
RT "Presence of a vertebrate fibrinogen-like sequence in an echinoderm.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2097-2101(1990).
CC -!- SIMILARITY: RELATED TO THE C-TERMINAL PART OF THE BETA AND GAMMA
CC CHAINS OF FIBRINOGEN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M31326; AAA29962.1; -
DR PIR; A35084; A35084.
DR HSSP; P02671; LFZD.
DR INTERPRO; IPR002181; -
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 282 FIBRINOGEN-LIKE PROTEIN A.
FT DISULFID 70 101
FT DISULFID 224 240 BY SIMILARITY.
SQ SEQUENCE 282 AA; 32280 MW; 07326C8865B7D3A2 CRC64;

Query Match 18.8%; Score 446; DB 1; Length 282;
Best Local Similarity 43.2%; Pred. No. 1.2e-23;
Matches 99; Conservative 33; Mismatches 75; Indels 22; Gaps 9;

QY 211 KDCSDYY--AIGK--SSEYRVTPDPKNSFEYVCMETMGGWTLQARLDGSTNFT 267
DB 68 RCDYDLQSCSQSPSGQYQTPDCGN-LIKYVCMETDEGWTVPQRIDGTINFYRS 126

QY 268 WQYKAGFGLNREFWGLNDKIHLLTKSEMLIRLDLPNGVELYALYQFYVANEFLK 327
DB 127 WSYQTGFCNLNTEFWGLNDNIHLYTSQGYELRVELNLTGNHYAKYKFRIGDSFSE 186

QY 328 YRLHVGNYGTAGDALRFNKHNDLKFPTTPDKNDPRPGNCGLYSSG---WTFDAC 384
DB 187 YLLVLGAYSGTAGDSLAY-----HNTMRFSTYDNDNDVY-SINCASHSSYGRGAWMYKSC 240

QY 385 LSNLNGKYYHOKYRGVRNGIFWGTWPGVSEAHPGYKSKFEAKMMIR 433
DB 241 LLSNLNGQYY--DYSGAPS-IWSYLPQDNDQIP-----FAEMKLNRN 280

RESULT 13
FIBA_RAT STANDARD; PRT; 782 AA.
ID FIBA_RAT
AC P06399;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR.
GN FGA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.

Fu Y., Cao Y., Hertzberg K., Grieninger G.;
Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A. (ALPHA FORM).
RX MEDLINE=86011580; PubMed=4046033;
RA Crabtree G.R., Comeau C.M., Fowlkes D.M., Fornace A.J. Jr.,
RA Malley J.D., Kant J.A.;
RT "Evolution and structure of the fibrinogen genes. Random insertion of
RT introns or selective loss?";
RL J. Mol. Biol. 185:1-19(1985).
RN [3]
RN SEQUENCE OF 20-36.
RP Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [4]
RN SEQUENCE OF 458-550 FROM N.A. (ALPHA FORM).
RC STRAIN=WTST; TISSUE=LIVER;
RX MEDLINE=87134033; PubMed=3817019;
RA Sobczak J., Lotti A.-M., Taroux P., Duquet M.;
RT "Molecular cloning of mRNA sequences transiently induced during rat
RT liver regeneration.";
RL Exp. Cell Res. 169:47-56(1987).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL MODULE.
CC DIVERGING FROM THIS MODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
CC CONNECT THE CENTRAL MODULE TO THE DISTAL MODULES CONTAINING THE
CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
CC ENDS OF THE ALPHA CHAINS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA; ARE
CC PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
CC PREDOMINANT FORM.
CC -!- PTM: THE ALPHA CHAIN IS NOT GLYCOSYLATED.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -----
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CC -----
CC EMBL; X86561; CAA60264.1; -
DR EMBL; X86561; CAA60263.1; -
DR EMBL; X85601; AAA41158.1; -
DR PIR; A03119; FGTA.
DR HSSP; P02671; LFZD.
DR INTERPRO; IPR002181; -
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Signal; Alternative splicing.
FT SIGNAL 1 19
FT PEPTIDE 20 36 FIBRINOPEPTIDE A.
FT CHAIN 20 782 FIBRINOGEN ALPHA-E CHAIN
FT SITE 36 37 CLEAVAGE (BY THROMBIN); RELEASE
FT FIBRINOPEPTIDE A).
FT DISULFID 48 48 INTERCHAIN (WITH C-48') (BY SIMILARITY).
FT DISULFID 56 56 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT DISULFID 65 65 INTERCHAIN (WITH C-49 IN GAMMA)
FT (BY SIMILARITY).
FT DISULFID 69 69 INTERCHAIN (WITH BETA) (BY SIMILARITY).


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FT DISULFID 181 INTERCHAIN (WITH C-165 IN GAMMA)
FT DISULFID 185 (BY SIMILARITY).
FT DISULFID 185 INTERCHAIN (WITH BETA) (BY SIMILARITY).
FT DISULFID 404 BY SIMILARITY.
FT VARSPLIC 547 DCDD -> GIHA (IN ISOFORM ALPHA).
FT VARSPLIC 551 MISSING (IN ISOFORM ALPHA).
FT VARSPLIC 551 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 30 EAGD -> DEGAG (IN REF. 3).
FT CONFLICT 140 Q -> E (IN REF. 2).
FT CONFLICT 212 D -> E (IN REF. 2).
FT CONFLICT 270 ASRGDLP -> LREEIYQ (IN REF. 2).
FT CONFLICT 473 S -> K (IN REF. 4).
SQ SEQUENCE 782 AA; 86685 MW; 744834DAE76D34C2 CRC64;.

Query Match 18.5%; Score 441; DB 1; Length 782;
Best Local Similarity 31.0%; Pred. No. 1e-22;
Matches 118; Conservative 61; Mismatches 116; Indels 86; Gaps 16;

QY 125 VGNRVRELESEVKNLSSELKNAKE--EINVLIH---GRLEKLNLMNMNIENYVDSKVAN 179
Db 413 LGNDGHEVYKEV-VTSDGSDCGDGMGLGTHSFSGRLDELSRMH-PELAGSFYDSRFGS 470
QY 180 LTFVNSLDGKCKPCSQEQIOQSRPVQHL-TYKDCSDYVYAGKRSEYRYVTPD----- 232
Db 471 LTSNFKFGSKTSDSDIFTDIEN-PSSHVPFSSSKTSTVRKQVTKSKYKMADEAASEAH 529
QY 233 -----PKNSS-FEYVCDMETMGGWT 252
Db 530 QEGDTRTKGRARTMRDCDDVLQTHPSGAQNGIFSIKPGSSKIFSVYVCDQETSLGGWL 589
QY 253 VLQARLDGNTFTWQDYKAGFNL-----RREFWLGNDKTHLLTKSKEMILRIDLEFN 308
Db 590 LIOQMDGSLNFNTWQDYKRGFGSLNDKGEFEWLGNDYLLHLLT-LRGSVLRLVELEDWA 648
QY 309 GVELYALYDQFYVANEFLKYLRLHVGNYGTAGDAL-----RFNKHYHDLKFFTPDKD 362
Db 649 GKEAYET-HFRVGEAEYALQVSSVQGTAGDALMEGSVEGTEYTSHSNNQFSTFDD 707
QY 363 NDYRPSGNCGLYSSGWMFADACLSANLNGKYY-----HQYRGVNRNGIFWGTWPGV 413
Db 708 ADQWEE-NCAEYVGGWYNSQANLNGIYYPGGTYDPRNNSPYE-IENGVLVWVPPFGA 765
QY 414 SEAHPGYKSKFKAQMIRP 434
Db 766 D-----YSLWAVRMKIRP 778
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RESULT 14
FIBG_PETMA STANDARD; PRT; 432 AA.
AC P04115;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIBRINOGEN GAMMA CHAIN PRECURSOR.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85199776; PubMed=2581603;
RA Strong D.D., Moore M., Cottrell B.A., Bohonus V.L., Pontes M.,
RA Evans B., Riley M., Doolittle R.F.;
RT "Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and
RT general characterization.";
RL Biochemistry 24:92-101(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC -1- POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC 4- THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
```

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CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
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CC -----
DR EMBL; K03049; AAA49262.1; .
DR PIR; A03129; FGLMGS.
DR HSSP; P02679; 1FIC.
DR INTERPRO; IPR002181; .
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 432 FIBRINOGEN GAMMA CHAIN.
FT DISULFID 32 32 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 42 42 INTERCHAIN (WITH THE BETA CHAIN)
FT DISULFID 46 46 INTERCHAIN (WITH THE ALPHA CHAIN)
FT DISULFID 158 158 INTERCHAIN (WITH THE BETA CHAIN)
FT DISULFID 162 162 INTERCHAIN (WITH THE GAMMA CHAIN)
FT DISULFID 178 207 BY SIMILARITY.
FT DISULFID 348 361 BY SIMILARITY.
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 432 AA; 49203 MW; B503979B296DFB24 CRC64;

Query Match 18.0%; Score 428.5; DB 1; Length 432;
Best Local Similarity 33.8%; Pred. No. 3.3e-22;
Matches 114; Conservative 46; Mismatches 132; Indels 45; Gaps 14;

QY 127 DNKRVRELESEVKNLSSE--LKNAAKEEINVLHGRLEKLNLMNMNIENYVDSKVANLTFEV 184
Db 90 DVRIITDEAIIKDSQKTVQKILEVRI-----LEQIGVSHDAQIOELSEMVRVNOQFVT 145
QY 185 N-----SLDGKCKPCSQEQIOQSRPVQHLIYKDCSDYVYAGKRSEYRYVTPDPKNSSF 238
Db 146 RLQQQLVDIRQTCSR--SCQDITANKISPIITGKCCQVVDNGGKDSGLYIKPLKAKQPF 203
QY 239 EYVCDMETMGGWTVLQARLDGSTNTRWQDYKAGFG-----NLRREFWLGNDKIHLLTK 294
Db 204 LVFCEIEN-GNGWTVIQHRHDSVNFTRDWSYREGFGYLAFTLTTFEFLWLNKEIHLLTG 262
QY 295 SEMILRIDLEDFNGVELYALYDQFYVANEFLKYLRLHVGNY-NGTAGDAL-----RF 345
Db 263 QQAYRLRIDLTWENTHRYADYGHFKLTPESEDEYRLFYSWYLDGDAGNAGDFGDDQ 322
QY 346 NKHYHNDL-KFFTTPDKDNDRYPSGNCGLYSSGWMFADACLSANLNGKYYH-QYRGV-- 401
Db 323 DKFYTHLGMLEFSTPERDNDKY-EGSCAEDQSGSWMNRCHAGHLNGKYFYFGNYRKTVD 381
QY 402 ----RNGIFWGTWPGVSEAHPGYKSKFKAQMIRP 434
Db 382 EFPYDDGLIWAATW-----HWRWY--SLKMTTMKLLP 410

RESULT 15
FIBG_CHICK .
ID FIBG_CHICK STANDARD; PRT; 741 AA.
AC P14448;
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01-JAN-1990 (Rel. 13, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FIBRINOGEN.ALPHA/ALPHA-E CHAIN PRECURSOR.
GNA.
GNA.
Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE OF 1-4 FROM N.A.
RA Greininger G.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 5-741 FROM N.A.
RX MEDLINE=90311369; PubMed=2367530;
RA Weissbach L., Grieninger G.;
RT "Bipartite mRNA for chicken alpha-fibrinogen potentially encodes an
amino acid sequence homologous to beta- and gamma-fibrinogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5198-5202(1990).
RN [3]
RP SEQUENCE OF 19-33
RX MEDLINE=78187470; PubMed=656462;
RA Takagi T., Finlayson J.S., Iwanaga S.;
RT "Amino acid sequence of chicken fibrinopeptide A.";
RL Biochim. Biophys. Acta 534:161-164(1978).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA: ARE
PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
PREDOMINANT FORM.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

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DR EMBL; U20803; AAB60686.1; JOINED.
DR EMBL; U20799; AAB60686.1; JOINED.
DR EMBL; U20800; AAB60686.1; JOINED.
DR EMBL; U20801; AAB60686.1; JOINED.
DR EMBL; U20802; AAB60686.1; JOINED.
DR EMBL; U20803; AAB60685.1; JOINED.
DR EMBL; U20799; AAB60685.1; JOINED.
DR EMBL; U20800; AAB60685.1; JOINED.
DR EMBL; U20801; AAB60685.1; JOINED.
DR EMBL; U20802; AAB60685.1; JOINED.
DR EMBL; M34096; AAA99306.1; JOINED.
DR EMBL; M34096; AAA99307.1; JOINED.
DR HSSP; P02671; 1F2D.
DR INTERPRO; IPR002181; .
DR PFAM; PF00147; fibrinogen_C; 1.
DR PROSITE; PS00514; FIBRIN_AC_C-DOMAIN; 1.
KW Blood coagulation; Plasma; Signal; Alternative splicing.
FT SIGNAL 1 18
FT PEPTIDE 19 33 FIBRINOPEPTIDE A.
FT CHAIN 34 741 FIBRINOGEN ALPHA-E CHAIN.
FT MOD_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 46 46 INTERCHAIN (WITH C-42') (BY SIMILARITY).
FT DISULFID 55 55 INTERCHAIN (WITH THE BETA CHAIN)
(BY SIMILARITY).
FT DISULFID 64 64 INTERCHAIN (WITH THE GAMMA CHAIN)
(BY SIMILARITY).

FT	DISULFID	68	68	INTERCHAIN (WITH THE BETA CHAIN) (BY SIMILARITY).
FT <td>DISULFID</td> <td>180</td> <td>180</td> <td>INTERCHAIN (WITH THE GAMMA CHAIN) (BY SIMILARITY).</td>	DISULFID	180	180	INTERCHAIN (WITH THE GAMMA CHAIN) (BY SIMILARITY).
FT <td>DISULFID</td> <td>184</td> <td>184</td> <td>INTERCHAIN (WITH THE BETA CHAIN) (BY SIMILARITY).</td>	DISULFID	184	184	INTERCHAIN (WITH THE BETA CHAIN) (BY SIMILARITY).
FT <td>DISULFID</td> <td>310</td> <td>341</td> <td>INTERCHAIN (WITH THE BETA CHAIN) (BY SIMILARITY).</td>	DISULFID	310	341	INTERCHAIN (WITH THE BETA CHAIN) (BY SIMILARITY).
FT <td>DISULFID</td> <td>33</td> <td>34</td> <td>CLEAVAGE (BY THROMBIN; RELEASE FIBRINOPEPTIDE A).</td>	DISULFID	33	34	CLEAVAGE (BY THROMBIN; RELEASE FIBRINOPEPTIDE A).
FT <td>VARSPPLIC</td> <td>506</td> <td>509</td> <td>DCDD -> GTOK (IN ISOFORM ALPHA).</td>	VARSPPLIC	506	509	DCDD -> GTOK (IN ISOFORM ALPHA).
FT <td>VARSPPLIC</td> <td>510</td> <td>741</td> <td>MISSING (IN ISOFORM ALPHA).</td>	VARSPPLIC	510	741	MISSING (IN ISOFORM ALPHA).
SO	SEQUENCE	741 AA;	82438 MW;	A09F5F4F186DE3A6 CRC64;

Query Match 18.0%; Score 427.5; DB 1; Length 741;
Best Local Similarity 39.2%; Pred. No. 7.8e-22;
Matches 96; Conservative 39; Mismatches 77; Indels 33; Gaps 11;

Qy	211	KDCSDY---YAIGKRSSSEYRVTPDPKNSSEFYVCDMETMGGVTVLQARLDGSTNFTRT	267
Db	505	KCDDIRQKHTSGAKSG-IFKIKPSGSKVLSVYCDQETTLGGWLLIQORMDGSVNFNT	563
Qy	268	WDYKAGFGNL-----RRFWLGNKIHLLTSKEMILRIDLEDFNGVELYALYDOFYVAN	323
Db	564	WDYRRGFGSDGKGQGLWLGNIHLLTQN-DTLRVELEDWDGNAAYAEY-IVQVGT	621
Qy	324	EFLXVRLHGVNNGTAGDAL-----RENKYNHDLKFTTPDKNDNDYPSGNCGLYSS	377
Db	622	EAEGYALTYSSEYEGTAGDALVAGWLEEGSEYTSQAOMQFSTFDRDDHWE-SCAEVYGG	680
Qy	378	GWFDACLSANLNGKY---HOKYR-----GVRNGIFWCTPGVSEAHPPGGYKSSFKEAK	429
Db	681	GWYNSCOAANLNGIYYPGGHYDPYVNPVYEIENGWVWIPF-----RASDY--SLKVVR	732
Qy	430	MMIRP 434	
Db	733	MKIRP 737	

Search completed: February 27, 2001, 12:52:02
Job time: 233 sec